



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 137736

TO: Bao-Qun Li
Location: rem/3d24/3c18
Art Unit: 1648
Wednesday, November 17, 2004
Case Serial Number: 10/784537

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

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Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:14:16 ; Search time 53.6504 Seconds
(without alignments)
96.503 Million cell updates/sec

Title: US-10-784-537-2
Perfect score: 57
Sequence: 1 CPRECECIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	82.5	425	2 Q8YUN1	Q8yuni anabaena sp
2	46	80.7	336	2 Q7UZU5	Q7uzu5 prochloroc
3	45	78.9	352	2 Q8GLI4	Q8gli4 synechococ
4	42	73.7	146	2 Q6IKM6	Q6ikm6 drosophila
5	42	73.7	210	2 Q89243	Q89243 marek's dis
6	42	73.7	210	2 Q782P9	Q782p9 gallid herp
7	42	73.7	348	2 Q7U4K2	Q7u4k2 synechococ
8	41	71.9	181	2 Q722D2	Q722d2 homo sapien
9	41	71.9	273	2 Q20000	Q20000 caenorhabdi
10	41	71.9	631	2 Q7RDG3	Q7rdg3 plasmodium
11	41	71.9	649	2 Q7MBG7	Q7mbg7 wolinnella s
12	40	70.2	295	2 Q7UVH5	Q7uvh5 rhodospirell
13	40	70.2	387	2 Q6UXQ3	Q6uxq3 homo sapien
14	40	70.2	387	2 A4Q8617	A4q8617 homo sapi
15	40	70.2	395	2 Q55456	Q55456 synechocyt
16	40	70.2	486	2 Q8ZA69	Q8za69 streptomyce
17	40	70.2	487	2 Q6GCL6	Q6gcl6 staphylococ
18	40	70.2	487	2 Q6GJK1	Q6gjk1 staphylococ
19	40	70.2	487	2 Q8NY13	Q8ny13 staphylococ
20	40	70.2	487	2 Q8S2Z0	Q8s2z0 streptomyce
21	40	70.2	487	2 Q39WD0	Q39wd0 staphylococ
22	40	70.2	487	2 Q7A7D2	Q7a7d2 staphylococ
23	40	70.2	488	2 Q3CDD4	Q3cdd4 mycobacteri
24	40	70.2	488	2 Q7MNS5	Q7mns5 vibrio vuln
25	40	70.2	489	2 Q87SE1	Q87se1 vibrio para
26	40	70.2	489	2 Q3DEN3	Q3den3 vibrio vuln
27	40	70.2	530	2 Q7Q460	Q7q460 anopheles g
28	40	70.2	552	2 Q8HXE2	Q8hxe2 macaca fasc
29	40	70.2	592	2 Q9XYA4	Q9xya4 strongyloce
30	40	70.2	630	2 Q6S5L8	Q6s5l8 homo sapien
31	40	70.2	630	2 Q81YW3	Q81yw3 homo sapien

32 40 70.2 630 2 AAR19363 Aar19363 homo sapi
33 40 70.2 662 2 Q9VSK1 Q9vsk1 drosophila
34 40 70.2 815 2 Q96JS2 Q96js2 homo sapien
35 40 70.2 816 1 NEL2 HUMAN Q99435 homo sapien
36 40 70.2 816 1 NEL2 CHICK Q90827 gallus gall
37 40 70.2 1188 2 Q9FKN9 Q9fkn9 arabidopsis
38 40 70.2 3133 1 HMCT BOWMO P98092 bombyx mori
39 39 68.4 95 2 Q8AXC3 Q8axc3 xenopus lae
40 39 68.4 211 1 UL45 GARHV P22652 gallid herp
41 39 68.4 211 1 UL45 GARHV P22653 gallid herp
42 39 68.4 211 2 Q77NR7 Q77mr7 meleagrid h
43 39 68.4 211 2 AAF66780 Aaf66780 turkey he
44 39 68.4 211 2 AAG14238 Aag14238 turkey he
45 39 68.4 211 2 AAS01688 Aas01688 turkey he

ALIGNMENTS

RESULT 1

Q8YUN1 PRELIMINARY; PRT; 425 AA.
AC Q8YUN1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alr2308 protein.
GN OrderedLocusNames=alr2308;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP MEDLINE=21595285; PubMed=11759840;
RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003589; BAB74007.1; -.
DR PIR; AE2094; AE2094.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR PROSITE; PRO0353; 4FE4SFDRDXIN.
DR PROSITE; PS00198; 4FE4S_FERREDXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 425 AA; 46348 MW; 7237DCE3EPD6912E CRC64;

Query Match 82.5%; Score 47; DB 2; Length 425;

Best Local Similarity 77.8%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9

Db 112 CPRPCEKIC 120

RESULT 2

Q7UZU5 PRELIMINARY; PRT; 336 AA.
AC Q7UZU5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PMW1560;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).

OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
OC	Prochlorococcus.
OC	NCBI_TaxID=59919;
RN	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA	Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA	Almgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA	Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA	Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA	Webb E.A., Zinser E.R., Chisholm S.W.;
RT	"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT	niche differentiation.";
RL	Nature 424:1042-1047(2003).
RL	EMBL; BX572094; CAE20019.1; -.
DR	GO; GO:0005489; F:electron transporter activity; IEA.
DR	GO; GO:0005506; F:iron ion binding; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.
DR	Pfam; PF00037; Fer4; 1.
DR	PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW	4Fe-4S; Complete proteome; Hypothetical protein; Iron; Iron-sulfur;
KW	Metal-binding.
SQ	SEQUENCE 336 AA; 37282 MW; CEC53CA6F8A27AB3 CRC64;
Query Match 80.7%; Score 46; DB 2; Length 336;	
Best Local Similarity 77.8%; Pred. No. 14;	
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 CPRECSIC 9
Db	103 CPRPCERIC 111
RESULT 3	
Q8GLI4	
ID	Q8GLI4 PRELIMINARY; PRT; 352 AA.
AC	Q8GLI4;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Light dependent period.
GN	Name=ldpa;
OS	Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OC	NCBI_TaxID=1140;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=PCC 7942;
RC	MEDLINE=22450571; PubMed=12562813;
RA	Katayama M., Kondo T., Xiong J., Golden S.S.;
RT	"ldpa encodes an iron-sulfur protein involved in light-dependent
RT	modulation of the circadian period in the cyanobacterium Synechococcus
RT	elongatus PCC 7942.";
RL	J. Bacteriol. 185:1415-1422(2003).
RL	EMBL; AY136759; AAN06910.1; -.
DR	GO; GO:0005489; F:electron transporter activity; IEA.
DR	GO; GO:0005506; F:iron ion binding; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.
DR	Pfam; PF00037; Fer4; 1.
DR	PROSITE; PS00353; 4FE4SPRDOXIN.
DR	PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW	4Fe-4S; Iron; Iron-sulfur; Metal-binding.
SQ	SEQUENCE 352 AA; 37865 MW; 33614612158F2936 CRC64;
Query Match 78.9%; Score 45; DB 2; Length 352;	
Best Local Similarity 66.7%; Pred. No. 21;	
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 CPRECSIC 9
Db	101 CPRPCERC 109

Query Match 73.7%; Score 42; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIS 9
||| | : ||
Db 161 CPRTCTAIC 169

RESULT 6
Q782P9 PRELIMINARY; PRT; 210 AA.
AC Q782P9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE UL45 protein.
GN Name=UL45;
OS Gallid herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=35250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPRS24;
RA Izumiya Y., Jang H., Ono M., Mikami T.;
RT "A Complete Genomic DNA Sequence of Marek's Disease Virus Type 2,
RT Strain HPRS24.";
RL Curr. Top. Microbiol. Immunol. 0:0-0(2000).
DR EMBL; AB049735; BAB16555.1; -;
DR InterPro; IPR009817; Varicello UL45.
DR Pfam; PF07144; Varicello UL45; 1.
SQ SEQUENCE 210 AA; 23038 MW; 6ED41E888FC10E53 CRC64;

Query Match 73.7%; Score 42; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIS 9
||| | : ||
Db 161 CPRTCTAIC 169

RESULT 7
Q7U4K2 PRELIMINARY; PRT; 348 AA.
AC Q7U4K2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative ldpA protein.
GN OrderedLocusNames=SYNW2065;
OS Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synecococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569694; CAE08580.1; -;
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR Nature 424:1037-1042(2003).
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 348 AA; 37531 MW; 1B1903E684081A95 CRC64;

Query Match 73.7%; Score 42; DB 2; Length 348;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIS 9
||| | : ||
Db 107 CFPQCQRCV 115

RESULT 8
Q7Z2D2 PRELIMINARY; PRT; 181 AA.
AC Q7Z2D2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hematological and neurological expressed protein 1B (Hematological and
DE neurological expressed gene 1-like protein variant b).
GN Name=HNI; Synonyms=HNIA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Guo J., Yu L.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wang J., Zhou G., Yu L., Zhao S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY322169; AAP83838.1; -;
DR EMBL; AF348672; AAP83962.1; -;
SQ SEQUENCE 181 AA; 19916 MW; FF644A114D288950 CRC64;

Query Match 71.9%; Score 41; DB 2; Length 181;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIS 9
||| | : ||
Db 152 CPERCRSVC 160

RESULT 9
Q20000 PRELIMINARY; PRT; 273 AA.
AC Q20000;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein F35A5.4.
GN ORFNames=F35A5.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Leimbach D.;
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

RA Waterston R.;
 RL EMBL; U46675; AAB52645.1; -;
 DR PIR; T16246; T16246.
 DR WormPep; F35A5.4; CE04488.
 DR InterPro; IPR003341; DUF139.
 DR Pfam; PF02363; Ctriplex; 9.
 KW Hypothetical protein.
 SQ SEQUENCE 273 AA; 29231 MW; 11542812CC566530 CRC64;

Query Match 71.9%; Score 41; DB 2; Length 273;
 Best Local Similarity 44.4%; Pred. No. 76;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPRECSIC 9
 ||:|:|
 Db 146 CPQCCQPCVC 154

RESULT 10
 Q7RDG3 PRELIMINARY; PRT; 631 AA.
 AC Q7RDG3;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE Delta-aminolevulinic acid synthetase.
 GN Name=PY05459;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=12368865;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow J.D., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser F.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 CC Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

CC EMBL; AABL01001737; EAA17486.1; -;
 DR GO; GO:0003870; F5-aminolevulinic synthase activity; IEA.
 DR GO; GO:0004883; F5-aminolevulinic synthase activity; IEA.
 DR GO; GO:0009058; P:biogenesis; IEA.
 DR GO; GO:0006783; P:heme biosynthesis; IEA.
 DR InterPro; IPR010961; S-aminolev synth.
 DR InterPro; IPR003408; Ala synthase.
 DR InterPro; IPR004839; Amino-trans-I/II.
 DR InterPro; IPR001917; Amino-trans-II.
 DR Pfam; PF02490; Ala synthase; 1.
 DR Pfam; PF00155; Amino-tran 1 2; 1.
 DR TIGRfams; TIGR01821; S-aminolev synth; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN 1.
 SQ SEQUENCE 631 AA; 72951 MW; D266BDE7255CD842 CRC64;

Query Match 71.9%; Score 41; DB 2; Length 631;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPRECSIC 9
 ||:|:|
 Db 555 CPQCKKCIC 563

RESULT 11
 Q7MBG7 PRELIMINARY; PRT; 649 AA.

AC Q7MBG7;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATEDEHYDROGENASE (EC
 1.2.1.43)).
 GN Name=FDHB; OrderedLocusNames=WS0477;
 OS Wolinella succinogenes.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Wolinella.
 OX NCBI_TaxID=844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSMZ 1740;
 RX MEDLINE=22882897; PubMed=14500908;
 RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
 RA Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
 RA Meyer P., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of Wolinella succinogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL; BX571658; CAE09617.1; -;
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR InterPro; IPR000759; Adrndx_reductase.
 DR InterPro; IPR001327; FAD_pyr_redox.
 DR InterPro; IPR000103; Pyridine_redox_2.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00469; PNDRTASEII.
 KW Complete proteome; Oxidoreductase.

SQ SEQUENCE 649 AA; 72557 MW; CCALE7589E36650D CRC64;
 Query Match 71.9%; Score 41; DB 2; Length 649;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECSIC 9
 ||:|:|
 Db 198 CPHPCESAC 206

RESULT 12
 Q7UVH5 PRELIMINARY; PRT; 295 AA.

AC Q7UVH5;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RB2632;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294137; CAD72749.1; -;
 DR InterPro; IPR004619; Baf.
 DR Pfam; PF03309; Bvg_acc_factor; 1.

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DR  TIGRFAMS; TIGR00671; baf: 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 295 AA; 31445 MW; 430B95673709B7A2 CRC64;

Query Match      70.2%; Score 40; DB 2; Length 295;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  3 RECESIC 9
Db  89 RECESVC 95

RESULT 13
Q6UXQ3
ID  Q6UXQ3 PRELIMINARY; PRT; 387 AA.
AC  Q6UXQ3
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  LPAL6438.
GN  ORFNames=UNQ6438;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=12975309;
RA  Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA  Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA  Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA  Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA  Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA  Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA  Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA  Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA  Godowski P.;
RT  "The secreted protein discovery initiative (SPDI), a large-scale
RT  effort to identify novel human secreted and transmembrane proteins: a
RT  bioinformatics assessment.";
RL  Genome Res. 13:2265-2270(2003).
DR  EMBL; AY358250; AAQ88617.1; -.
SQ  SEQUENCE 387 AA; 42782 MW; 558D4E2167B69AF7 CRC64;

Query Match      70.2%; Score 40; DB 2; Length 387;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  1 CPRECECIC 9
Db  161 CPIQCEKLC 169

RESULT 15
Q55456
ID  Q55456 PRELIMINARY; PRT; 395 AA.
AC  Q55456;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  S110031 protein.
GN  OrderedLocustNames=s110031;
OS  Synchocystis sp. (strain PCC 6803).
OC  Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX  NCBI_TaxID=1148;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=PCC6803;
RA  Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA  Miyajima N., Hiroseawa M., Sugiura M., Sasamoto S., Kimura T.,
RA  Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA  Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA  Tabata S.;
RT  "Sequence analysis of the genome of the unicellular cyanobacterium
RT  Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT  entire genome and assignment of potential protein-coding regions.";
RL  DNA Res. 3:109-136(1996).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96127529; PubMed=8590279;
RA  Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA  Sugiura M., Tabata S.;
RT  "Sequence analysis of the genome of the unicellular cyanobacterium
RT  Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT  region from map positions 64% to 92% of the genome.";
RL  DNA Res. 2:153-166(1995).
DR  EMBL; D64006; BAAL0799.1; -.
DR  PIR; S75952; S75952.
DR  HSP; P00193; 1DUR.
DR  GO; GO:0005489; F:electron transporter activity; IEA.
DR  GO; GO:0005506; F:iron ion binding; IEA.

```

DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 395 AA; 43410 MW; 077421437A6B0DC0 CRC64;

Query Match 70.2%; Score 40; DB 2; Length 395;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CPRECECIC 9
||| | :|
Db 131 CPRPCAQVC 139

Search completed: November 16, 2004, 14:29:46
Job time : 55.6604 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:09:48 ; Search time 74.0755 Seconds
(without alignments)
62.956 Million cell updates/sec

Title: US-10-784-537-3

Perfect score: 84

Sequence: 1 CPKVCPRCESNC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	84	100.0	13	5	ABG60452	PF	Abg60452 Selective
2	84	100.0	13	6	ABR56864	PF	Abt56864 Aminopept
3	51	60.7	762	6	ABU20893	PR	Abu20893 Protein e
4	50	59.5	9	5	ABG60448	PF	Abg60448 Selective
5	50	59.5	9	6	ABR56860	PF	Abt56860 Aminopept
6	50	59.5	13	2	AAW13427	PA	Aaw13427 Breast tu
7	50	59.5	13	2	AAW60290	PA	Aaw60290 Breast ca
8	50	59.5	13	2	AAW93627	PI	Aaw93627 Breast tu
9	50	59.5	13	3	AAU17959	XX	Aau17959 Integrin-
10	50	59.5	13	3	AAU17923	DR	Aau17923 VEGF anta
11	50	59.5	13	3	AAU21702	XX	Aau21702 Human bre
12	50	59.5	13	4	AAU06280	XX	Aau06280 Human bre
13	50	59.5	13	5	AAU81104	XX	Aau81104 Integrin-
14	50	59.5	13	5	ABR72956	PT	Abt72956 Integrin
15	50	59.5	13	7	ADJ73110	XX	Adj73110 Integrin
16	50	59.5	13	8	ADJ52745	XX	Adj52745 CHI delet
17	50	59.5	13	8	ADJ51706	XX	Adj51706 CHI delet
18	50	59.5	1364	5	ABG66755	XX	Abg66755 Human nov
19	50	59.5	1364	5	ABG66701	XX	Abg66701 Human nov
20	50	59.5	1594	7	ADJ69349	XX	Adj69349 Human hea
21	50	59.5	5703	8	ADL23265	XX	Adl23265 Human MOC
22	49	58.3	177	7	ADJ92337	XX	Adj92337 Mouse hai
23	48	57.1	64	3	AAU39289	XX	Aau39289 Gene 38 h
24	48	57.1	98	3	AAV65429	XX	Aav65429 Human 5'
25	48	57.1	121	4	AAW95477	XX	Aaw95477 Human rep

26	48	57.1	121	4	ABB96162	XX	Abb96162 Human tes
27	48	57.1	132	5	ABP69453	XX	Abp69453 Human pol
28	48	57.1	132	5	ABB89837	XX	Abb89837 Human pol
29	48	57.1	174	6	ABR41785	XX	Abt41785 Human DIT
30	47	56.0	31	5	ABG60450	XX	Abg60450 Selective
31	47	56.0	31	6	ABR56862	XX	Abt56862 Aminopept
32	47	56.0	383	3	AAU06124	XX	Aau06124 Drosophil
33	47	56.0	461	6	ABU24727	XX	Abu24727 Protein e
34	47	56.0	470	6	ABU24443	XX	Abu24443 Protein e
35	47	56.0	654	4	ABR63025	XX	Abt63025 Drosophil
36	47	56.0	2144	4	ABR62331	XX	Abt62331 Drosophil
37	46	54.8	103	5	AAO21297	XX	Aao21297 Wheat KCP
38	46	54.8	414	6	ABR43199	XX	Abt43199 Human REM
39	46	54.8	478	6	ABR43176	XX	Abt43176 Human REM
40	46	54.8	573	2	AAU80633	XX	Aau80633 Clone 3-2
41	46	54.8	1024	4	ABR69268	XX	Abt69268 Drosophil
42	46	54.8	2469	5	AAE18207	XX	Aae18207 Human MOL
43	46	54.8	2469	7	ADD18192	XX	Add18192 Human mol
44	46	54.8	2471	2	AAO27065	XX	Aao27065 Human Not
45	46	54.8	2471	2	AAU06816	XX	Aau06816 Human Not

ALIGNMENTS

RESULT 1
ABG60452
ID ABG60452 standard; peptide; 13 AA.

XX AC ABG60452;

XX DT 30-JUL-2002 (first entry)

XX DE Selective targeting peptide #127.

XX KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;

XX KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;

XX KW viral infection; cardiovascular disease; degenerative disease; ischaemia;

XX KW inflammation; macular degeneration; antiinflammatory; antidiabetic;

XX KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;

XX KW gene therapy.

XX OS Synthetic.

XX PN WO200220769-A1.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US027692.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-415731/44.

XX Targeting peptides identified by phage display, useful for targeting

XX delivery to an organ or tissue, particularly for treating a disease, e.g.

XX cancer, inflammatory or autoimmune diseases, infections or cardiovascular

XX disease.

XX Claim 22; Page 109; 317pp; English.

XX The invention relates to an isolated peptide of 100 amino acids or less

XX in size useful for targeting delivery to an organ or tissue, particularly

XX for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory

XX disease, atherosclerosis, autoimmune disease, bacterial infection, viral

XX infection, cardiovascular disease or degenerative disease. The peptide is

XX also useful for inducing apoptosis, particularly to a subject with

XX ischaemia, cancer, arthritis, diabetes, cardiovascular disease.

CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting
 CC peptides of the invention
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 84; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 |||||
 DB 1 CPKVCPRCESNC 13

RESULT 2
 ID ABR56864 standard; peptide; 13 AA.
 XX
 AC ABR56864;
 XX
 DT 30-JUL-2003 (first entry)
 XX
 DE Aminopectidase A (APA) binding peptide SEQ ID NO:60.
 XX
 KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipaeic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; aminopectidase A.
 OS Synthetic.
 XX

PN WO2003022991-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027836.
 XX
 PR 07-SEP-2001; 2001WO-US027692.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Pasqualini R, Arap W, Kolonin MG;
 XX
 DR WPI; 2003-371749/35.
 XX
 PT Treating obesity or a lipodystrophy comprises obtaining a targeting
 PT peptide selective for adipose tissue, attaching the peptide to a
 PT therapeutic agent to form a complex, and administering the complex to a
 PT subject.
 XX
 PS Example 8; Page 104; 247pp; English.
 XX
 CC The present invention describes a method for treating obesity or a
 CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
 CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
 CC agent to form a complex; (c) administering the complex to a subject; and
 CC (d) inducing weight loss in the subject or treating lipodystrophy. The
 CC adipose targeting peptides have anorectic and antilipaeic activities,
 CC and can be used in peptide and gene therapy. The method is used for
 CC treating obesity or a lipodystrophy that is related to infection with
 CC human immunodeficiency virus (HIV). The peptides used in the method can
 CC also be used for targeting delivery to an organ or tissue, such as
 CC placental delivery. A receptor that binds to a placenta targeting peptide
 CC is used to screen compounds for teratogenic activity. ABR56806 to
 CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 84; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 |||||
 DB 1 CPKVCPRCESNC 13

RESULT 3
 ID ABU20893 standard; protein; 762 AA.
 XX
 AC ABU20893;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #6420.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Bacteroides fragilis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX

PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.
 DR N-PSDB; ACA24763.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 48817; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 762 AA;
 Query Match 60.7%; Score 51; DB 6; Length 762;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 QY 1 CPKVCPR--CESNC 13
 Db 388 CGRVCPEKQCESKC 402
 :|||:|
 RESULT 4
 ID ABG60448 standard; peptide; 9 AA.
 XX AC ABG60448;
 XX DT 30-JUL-2002 (first entry)
 XX DE Selective targeting peptide #123.
 XX KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.
 XX OS Synthetic.
 XX WO200220769-A1.
 XX PD 14-MAR-2002.
 XX PF 07-SEP-2001; 2001WO-US027692.
 XX PR 08-SEP-2000; 2000US-0231266P.
 XX PR 17-JAN-2001; 2001US-00765101.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Arap W, Pasqualini R;
 XX WPI; 2002-415731/44.
 XX Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease, e.g.
 PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
 PT disease.
 XX Claim 22; Page 102; 317pp; English.
 XX The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting
 CC peptides of the invention

XX SQ Sequence 9 AA;
 Query Match 59.5%; Score 50; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CPRECESNC 13
 Db 1 CPRECESIC 9
 :|||:|
 RESULT 5
 ID ABR56860 standard; peptide; 9 AA.
 XX AC ABR56860;
 XX DT 30-JUL-2003 (first entry)
 XX DE Aminopeptidase A (APA) binding peptide SEQ ID NO:56.
 XX KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipaeamic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
 XX OS Synthetic.
 XX WO2003022991-A2.
 XX PD 20-MAR-2003.
 XX PF 30-AUG-2002; 2002WO-US027836.
 XX PR 07-SEP-2001; 2001WO-US027692.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Pasqualini R, Arap W, Kolonin MG;
 XX WPI; 2003-371749/35.
 XX Treating obesity or a lipodystrophy comprises obtaining a targeting
 PT peptide selective for adipose tissue, attaching the peptide to a
 PT therapeutic agent to form a complex, and administering the complex to a
 PT subject.
 XX Example 8; Page 98; 247pp; English.
 XX The present invention describes a method for treating obesity or a
 CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
 CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
 CC agent to form a complex; (c) administering the complex to a subject; and
 CC (d) inducing weight loss in the subject or treating lipodystrophy. The
 CC adipose targeting peptides have anorectic and antilipaeamic activities,
 CC and can be used in peptide and gene therapy. The method is used for
 CC treating obesity or a lipodystrophy that is related to infection with
 CC human immunodeficiency virus (HIV). The peptides used in the method can
 CC also be used for targeting delivery to an organ or tissue, such as
 CC placental delivery. A receptor that binds to a placenta targeting peptide
 CC is used to screen compounds for teratogenic activity. ABR56806 to
 CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
 CC exemplification of the present invention
 XX SQ Sequence 9 AA;
 Query Match 59.5%; Score 50; DB 6; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CPRECESNC 13
 :|||:|

```

Db          1 CPRECESIC 9

RESULT 6
AAW13427
ID AAW13427 standard; peptide; 13 AA.
XX
AC AAW13427;
XX
DT 15-JAN-1998 (first entry)
XX
DE Breast tumour homing peptide.
XX
KW Breast tumour homing peptide; cancer; in vivo panning; screening;
KW phage display; drug delivery.
OS Synthetic.
XX
PN WO9710507-A1.
PD 20-MAR-1997.
XX
PF 10-SEP-1996; 96WO-US014600.
XX
PR 11-SEP-1995; 95US-00526708.
PR 11-SEP-1995; 95US-00526710.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Ruoslahti E, Pasqualini R;
XX
DR WPI; 1997-202359/18.
XX
PT Obtaining compound that homes to selected organ or tissue - by in vivo
PT panning method, specifically to identify brain, kidney, angiogenic
PT vasculature or tumour tissue homing peptide(s).
XX
PS Claim 18; Page 68; 75pp; English.
XX
CC This synthetic peptide is a claimed example of a breast tumour-homing
CC peptide that was identified using a novel method for obtaining molecules
CC that home to a selected organ or tissue. This in vivo panning method
CC typically involves administering a phage display library to a subject,
CC and identifying expressed peptides which home to the desired organ or
CC tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue.
CC The isolated peptides (see AAW13412-52, AAW11181-86) can be used to
CC target e.g. drugs, toxins or labels to the selected organ/tissue
CC (claimed) or to identify and/or isolate target molecules (claimed). The
CC peptides can be directly identified in vivo, as compared to prior art in
CC vitro screening methods, which require further examination to see if they
CC maintain specificity in vivo
XX
SQ Sequence 13 AA;

Query Match 59.5%; Score 50; DB 2; Length 13;
Best Local Similarity 53.8%; Pred. No. 3.8;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
DB | : ||| : | : |
1 CGRECPRLCQSSC 13

RESULT 8
AAW93627
ID AAW93627 standard; protein; 13 AA.
XX
AC AAW93627;
XX
DT 28-JUN-1999 (first entry)
XX
DE Breast tumour homing peptide 1.
XX
KW Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
KW prognosis; inflammation; regeneration; wounded tissue; targeting;
KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
KW occlusive thrombus.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9913329-A1.
XX
PD 18-MAR-1999.
XX
PF 08-SEP-1998; 98WO-US018895.
XX
PR 10-SEP-1997; 97US-00926914.
PR 25-AUG-1998; 98US-00139802.

```

Tumour homing peptide; in vivo panning; breast carcinoma;
alpha-v-containing integrin binding motif; tumour.

Unidentified.

WO9810795-A2.

19-MAR-1998.

10-SEP-1997; 97WO-US016086.

10-SEP-1996; 96US-00710067.

(BURN-) BURNHAM INST.

Ruoslahti E, Pasqualini R;

WPI; 1998-207151/18.

Tumour homing molecules and their conjugates - useful for, e.g. directing
linked moiety to tumour containing angiogenic vasculature.

Disclosure; Page 6; 105pp; English.

The present peptide represents a tumour homing peptide, and is produced
by in vivo panning. The peptide homes to a breast carcinoma. The in vivo
panning comprises administering a library of diverse peptides to a
subject having a tumour, collecting a sample of the tumour, identifying a
peptide that homes to the tumour, collecting a sample of normal tissue
corresponding to the tumour, and determining that the peptide that homes
to the tumour is not present in the normal tissue. The tumour homing
peptide can be linked to a moiety (e.g. doxorubicin), and used to direct
the moiety to a tumour

Sequence 13 AA;

Query Match 59.5%; Score 50; DB 2; Length 13;
Best Local Similarity 53.8%; Pred. No. 3.8;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
| : ||| : | : |
1 CGRECPRLCQSSC 13

RESULT 8
AAW93627
ID AAW93627 standard; protein; 13 AA.

AC AAW93627;

DT 28-JUN-1999 (first entry)

DE Breast tumour homing peptide 1.

Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
prognosis; inflammation; regeneration; wounded tissue; targeting;
macular degeneration; diabetic retinopathy; rheumatoid arthritis;
occlusive thrombus.

OS Synthetic.
Mus sp.

PN WO9913329-A1.

PD 18-MAR-1999.

PF 08-SEP-1998; 98WO-US018895.

PR 10-SEP-1997; 97US-00926914.
25-AUG-1998; 98US-00139802.

XX (BURN-) BURNHAM INST.
 XX
 XX
 PI Ruoslahti E, Pasqualini R;
 XX
 XX
 DR WPI; 1999-215158/18.
 XX
 XX
 PT Identifying molecules that home to angiogenic vasculature used as targets
 PT for anticancer agents.
 XX
 XX
 PS Example II; Page 67; 180pp; English.
 XX
 CC This invention describes novel peptides which home to angiogenic
 CC vasculature, specifically of a tumour and which have anti-tumour, anti-
 CC inflammatory, anti-angiogenic and anti-arthritis activity. Such molecules
 CC are identified by treating a purified NGR receptor with a test compound
 CC and identifying compounds that bind specifically to the NGR receptor. The
 CC peptides of the invention are inhibitors of angiogenesis and can be used
 CC to produce conjugates for delivering agents to angiogenic vasculature,
 CC particularly anticancer drugs or an imaging agent, for diagnosis or
 CC prognosis. These conjugates may be directed to non-tumour angiogenic
 CC vasculature, e.g. that present in inflammatory, regenerating or wounded
 CC tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
 CC or rheumatoid arthritis. The peptides provide specific targeting to
 CC tumours, especially their supporting vasculature, since the NGR receptor
 CC is exposed to the circulation only in angiogenic vasculature. Precise
 CC targeting should reduce the systemic toxicity of anticancer drugs in the
 CC conjugates. Complete killing of all target cells may not be essential
 CC since partial denudation of endothelium may result in an occlusive
 CC thrombus, and endothelial cells are unlikely to become resistant to
 CC anticancer agents nor to lose the targeting receptor. AAW93622-W93809 and
 CC AAW93843-44 are examples of tumour homing peptides used in the invention
 XX
 XX Sequence 13 AA;
 SQ

Query Match 59.5%; Score 50; DB 2; Length 13;
 Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCECSNC 13
 Db 1 CGRCFRLCQSSC 13

RESULT 9
 AAB17959
 ID AAB17959 standard; peptide; 13 AA.
 XX
 AC AAB17959;
 XX
 XX 31-OCT-2000 (first entry)
 DT
 DE Integrin-binding peptide sequence SEQ ID NO:1071.
 XX
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US025044.
 PF
 XX 23-OCT-1998; 98US-0105371P.
 PR
 XX 22-OCT-1999; 99US-00428082.
 PR
 XX (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;

PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 XX WPI; 2000-350702/30.
 DR
 XX
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Claim 39; Page 589; 608pp; English.
 XX
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAW69443 to AAW69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 13 AA;
 SQ

Query Match 59.5%; Score 50; DB 3; Length 13;
 Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCECSNC 13
 Db 1 CGRCFRLCQSSC 13

RESULT 10
 AAB17923
 ID AAB17923 standard; peptide; 13 AA.
 XX
 AC AAB17923;
 XX
 XX 31-OCT-2000 (first entry)
 DT
 DE VEGF antagonist peptide sequence SEQ ID NO:1027.
 XX
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US025044.
 PF
 XX 23-OCT-1998; 98US-0105371P.
 PR
 XX 22-OCT-1999; 99US-00428082.
 PR
 XX (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 XX Claim 39; Page 557; 608pp; English.
 XX
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX Sequence 13 AA;
 SQ

Query Match 59.5%; Score 50; DB 3; Length 13;
 Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 | : ||| | : | : |
 Db 1 CGRCFRLCQSSC 13

RESULT 12
 AAE06280
 ID AAE06280 standard; peptide; 13 AA.
 XX AAE06280;
 AC
 XX 25-SEP-2001 (first entry)
 DT
 XX Human breast tumour homing peptide #1.
 DE
 XX Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
 KW antimicrobial peptide; prostate cancer; breast tumour homing molecule;
 KW cytostatic; human.
 XX Homo sapiens.
 OS
 XX WO200153342-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 16-JAN-2001; 2001WO-US001362.
 PF
 XX 21-JAN-2000; 2000US-00489582.
 PR
 XX (BURN-) BURNHAM INST.
 XX
 XX Ruoslahti EI, Pasqualini R, Arap W, Bredeesen DE, Ellerby HM;
 PI
 XX WPI; 2001-451901/48.
 DR
 XX Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
 PT prostate cancer, comprises a prostate-homing peptide linked to an
 PT antimicrobial peptide.
 PT
 XX Example 5; Page 89; 176pp; English.
 PS
 XX The patent discloses novel chimeric prostate-homing pro-apoptotic peptide
 CC which comprises a prostate-homing peptide linked to an antimicrobial
 CC peptide, where the chimeric peptide is selectively internalised by and
 CC exhibits high toxicity to prostate tissue and where the antimicrobial
 CC peptide has low mammalian cell toxicity when not linked to prostate-
 CC homing peptide. The chimeric peptide is used to direct an antimicrobial
 CC peptide in vivo to a prostate cancer, to induce selective toxicity in
 CC vivo in a prostate cancer, and to treat a patient with prostate cancer.
 CC The present sequence is human breast tumour homing peptide. This sequence
 CC is useful in the homing of pro-apoptotic conjugates of the invention
 XX Sequence 13 AA;
 SQ

Query Match 59.5%; Score 50; DB 3; Length 13;
 Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 | : ||| | : | : |
 Db 1 CGRCFRLCQSSC 13

RESULT 11
 AAB21702
 ID AAB21702 standard; peptide; 13 AA.
 XX AAB21702;
 AC
 XX 22-MAR-2001 (first entry)
 DT
 XX Human breast tumour homing peptide #2.
 DE
 XX Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
 KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
 KW
 XX Homo sapiens.
 OS
 XX WO200042973-A2.
 PN
 XX 27-JUL-2000.
 PD
 XX 21-JAN-2000; 2000WO-US001602.
 PF
 XX 22-JAN-1999; 99US-00235902.
 PR
 XX (BURN-) BURNHAM INST.
 XX
 XX Ellerby HM, Bredeesen DE, Pasqualini R, Ruoslahti EI;
 PI
 XX WPI; 2000-499174/44.
 DR
 XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that
 PT selectively homes to a mammalian cell type or tissue linked to an
 PT antimicrobial peptide, useful for the treatment of prostate cancer.
 PT
 XX Example 5; Page 90; 118pp; English.
 PS
 XX

The present invention relates to homing pro-apoptotic conjugates,
 comprising of a tumour homing molecule that selectively homes to a
 mammalian cell type or tissue, linked to an antimicrobial peptide. The
 homing pro-apoptotic conjugates are selectively internalised by the
 mammalian cell type or tissue and exhibits high toxicity, especially to
 angiogenic vasculature. The antimicrobial peptide has low mammalian cell
 toxicity when not linked to the tumor homing molecule. The conjugates are
 useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
 prostate cancer or melanoma. The present sequence is a homing peptide
 isolated in the present invention, which can be conjugated to an
 antimicrobial peptide to make the homing pro-apoptotic conjugates of the
 present invention
 Sequence 13 AA;
 Query Match 59.5%; Score 50; DB 3; Length 13;
 Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 | : ||| | : | : |
 Db 1 CGRCFRLCQSSC 13

RESULT 12
 AAE06280
 ID AAE06280 standard; peptide; 13 AA.
 XX AAE06280;
 AC
 XX 25-SEP-2001 (first entry)
 DT
 XX Human breast tumour homing peptide #1.
 DE
 XX Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
 KW antimicrobial peptide; prostate cancer; breast tumour homing molecule;
 KW cytostatic; human.
 XX Homo sapiens.
 OS
 XX WO200153342-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 16-JAN-2001; 2001WO-US001362.
 PF
 XX 21-JAN-2000; 2000US-00489582.
 PR
 XX (BURN-) BURNHAM INST.
 XX
 XX Ruoslahti EI, Pasqualini R, Arap W, Bredeesen DE, Ellerby HM;
 PI
 XX WPI; 2001-451901/48.
 DR
 XX Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
 PT prostate cancer, comprises a prostate-homing peptide linked to an
 PT antimicrobial peptide.
 PT
 XX Example 5; Page 89; 176pp; English.
 PS
 XX The patent discloses novel chimeric prostate-homing pro-apoptotic peptide
 CC which comprises a prostate-homing peptide linked to an antimicrobial
 CC peptide, where the chimeric peptide is selectively internalised by and
 CC exhibits high toxicity to prostate tissue and where the antimicrobial
 CC peptide has low mammalian cell toxicity when not linked to prostate-
 CC homing peptide. The chimeric peptide is used to direct an antimicrobial
 CC peptide in vivo to a prostate cancer, to induce selective toxicity in
 CC vivo in a prostate cancer, and to treat a patient with prostate cancer.
 CC The present sequence is human breast tumour homing peptide. This sequence
 CC is useful in the homing of pro-apoptotic conjugates of the invention
 XX Sequence 13 AA;
 SQ

Query Match 59.5%; Score 50; DB 4; Length 13;
 Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 | : ||| | : | : |
 Db 1 CGRECFRLCQSSC 13

RESULT 13

AAU81104
 ID AAU81104 standard; peptide; 13 AA.

XX
 AC AAU81104;

DT 09-APR-2002 (first entry)

DE Integrin-antagonist peptide #11.

XX IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
 KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
 KW echistatin; integrin; selectin; vinculin; platelet aggregation;
 KW angiogenesis; tumour; inflammation; autoimmune disease;
 KW rheumatoid arthritis; osteoporosis.

XX Synthetic.

XX WO200181377-A2.

PN 01-NOV-2001.

XX 23-APR-2001; 2001WO-US013069.

XX 21-APR-2000; 2000US-0198919P.

PR 03-MAY-2000; 2000US-0201394P.

XX (AMGE-) AMGEN INC.

XX Feige U, Kohno T, Lacey DL, Boone TC;

DR WPI; 2002-062025/08.

XX Composition comprising integrin or adhesion antagonistic peptide and
 PT vehicle, useful for treating or preventing platelet aggregation, has a
 PT longer half-life than free peptide.

XX Claim 11; Page 19; 68pp; English.

XX The invention relates to a composition comprising an integrin/adhesion
 CC antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
 CC based on laminin or saw-scaled viper echistatin and target integrin,
 CC selectin or vinculin. Also included are compounds of formula (Ia) and
 CC their multimers (X¹-1-(X²)_n where; F¹ = Fc domain; X¹ and X² =
 CC -(L¹)¹-c-p¹-1, (L¹)¹-c-p¹-1-(L²)₂-d-p², (L¹)¹-c-p¹-1-(L³)₃-e-
 CC p³ or (L¹)¹-c-p¹-1-(L²)₂-d-p²-1-(L³)₃-e-p³-1-(L⁴)₄-f-p⁴; F¹-p⁴ = same or
 CC provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
 CC an expression vector containing the nucleic acid, host cells containing
 CC the vector, producing a pharmaceutically active compound (B) by
 CC covalently linking at least one Fc domain to at least one amino acid
 CC sequence of a selected randomized (I) and any of six laminin-related
 CC peptides (Ib). The compositions are used prophylactically and
 CC therapeutically in the same way as (I), e.g. to inhibit platelet
 CC aggregation or angiogenesis (tumours), or to treat inflammation and
 CC autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
 CC of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
 CC domain) to (I) increases the half-life (free (I) are normally degraded
 CC very quickly in vivo). The present sequence is an antagonist peptide of
 CC the invention

XX Sequence 13 AA;

Query Match 59.5%; Score 50; DB 5; Length 13;

Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 | : ||| | : | : |
 Db 1 CGRECFRLCQSSC 13

RESULT 14

ABB72956
 ID ABB72956 standard; peptide; 13 AA.

XX
 AC ABB72956;

XX 05-APR-2002 (first entry)

DE Integrin binding peptide SEQ ID NO:1071.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TWP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antifertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX WO200183525-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

DR WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.

XX Claim 39; Page 47; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,

CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention

XX Sequence 13 AA;

Query Match 59.5%; Score 50; DB 5; Length 13;

Best Local Similarity 53.8%; Pred. No. 3.8;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CPKVCPRCESNC 13

| : ||| | : |

Db 1 CGRECPRLCQSSC 13

RESULT 15

ADJ73110

ID ADJ73110 standard; peptide; 13 AA.

XX AC ADJ73110;

XX DT 06-MAY-2004 (first entry)

XX DE Integrin binding peptide sequence SeqID 564.

XX XX

KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KW integrin.

XX OS Synthetic.

XX PN WO2003084477-A2.

XX PD 16-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US009139.

XX PR 29-MAR-2002; 2002US-0368791P.

XX PA (CENZ) CENTOCOR INC.

XX PI Heavner GA, Knight DM, Scallion BJ, Grayeb J;

XX DR WPI; 2003-804237/75.

XX PT New CDR mimetibody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.

PS Disclosure; SEQ ID NO 564; 97pp; English.

XX CC This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC peptide sequence is an integrin binding peptide sequence used to make a
 CC mimetibody of the invention.

XX SQ Sequence 13 AA;

Query Match 59.5%; Score 50; DB 7; Length 13;

Best Local Similarity 53.8%; Pred. No. 3.8;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CPKVCPRCESNC 13

| : ||| | : |

Db 1 CGRECPRLCQSSC 13

Search completed: November 16, 2004, 14:24:30

Job time : 78.0755 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:16:01 ; Search time 18.3962 Seconds
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46.865 Million cell updates/sec

Title: US-10-784-537-3

Perfect score: 84

Sequence: 1 CPKVCPRCESNC 13

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	50	59.5	13	US-09-139-802-2	Sequence 2, Appli
2	50	59.5	13	US-09-659-786-2	Sequence 2, Appli
3	50	59.5	13	US-08-926-914-2	Sequence 2, Appli
4	50	59.5	13	US-09-428-082B-1071	Sequence 1071, Ap
5	48	57.1	98	US-09-621-976-6330	Sequence 6330, Ap
6	47	56.0	58	US-09-270-767-57784	Sequence 57784, A
7	47	56.0	118	US-09-270-767-42488	Sequence 42488, A
8	47	56.0	383	US-08-857-076-105	Sequence 105, App
9	46	54.8	1015	US-08-537-210A-1	Sequence 1, Appli
10	46	54.8	1015	US-09-113-825-1	Sequence 1, Appli
11	46	54.8	2471	US-08-185-432-16	Sequence 16, Appl
12	46	54.8	2471	US-08-083-590A-19	Sequence 19, Appl
13	46	54.8	2471	US-08-532-384-19	Sequence 19, Appl
14	46	54.8	2471	US-08-899-232-1	Sequence 1, Appli
15	46	54.8	2471	US-09-121-457-1	Sequence 1, Appli
16	45	53.6	475	US-09-489-039A-13710	Sequence 13710, A
17	44	52.4	58	US-08-454-295-6	Sequence 6, Appli
18	44	52.4	58	US-08-454-295-7	Sequence 7, Appli
19	44	52.4	58	US-08-454-295-8	Sequence 8, Appli
20	44	52.4	58	US-09-431-500A-6	Sequence 6, Appli
21	44	52.4	58	US-09-431-500A-7	Sequence 7, Appli
22	44	52.4	58	US-09-431-500A-8	Sequence 8, Appli
23	44	52.4	58	US-09-431-498-6	Sequence 6, Appli
24	44	52.4	58	US-09-431-498-7	Sequence 7, Appli
25	44	52.4	58	US-09-431-498-8	Sequence 8, Appli
26	44	52.4	58	US-09-431-499-6	Sequence 6, Appli
27	44	52.4	58	US-09-431-499-7	Sequence 7, Appli

28	44	52.4	58	4	US-09-431-499-8	Sequence 8, Appli
29	44	52.4	77	4	US-09-270-767-56916	Sequence 56916, A
30	44	52.4	163	4	US-09-513-999C-4416	Sequence 4416, Ap
31	44	52.4	368	3	US-08-454-295-3	Sequence 3, Appli
32	44	52.4	368	3	US-09-431-500A-3	Sequence 3, Appli
33	44	52.4	368	4	US-09-431-498-3	Sequence 3, Appli
34	44	52.4	368	4	US-09-431-499-3	Sequence 3, Appli
35	44	52.4	370	3	US-08-857-076-104	Sequence 104, App
36	44	52.4	429	4	US-09-270-767-42636	Sequence 42636, A
37	44	52.4	478	4	US-09-134-000C-5543	Sequence 5543, Ap
38	44	52.4	480	4	US-09-710-279-2852	Sequence 2852, Ap
39	44	52.4	480	4	US-09-710-279-2986	Sequence 2986, Ap
40	44	52.4	490	3	US-09-134-001C-4019	Sequence 4019, Ap
41	44	52.4	1382	2	US-08-737-715-2	Sequence 2, Appli
42	44	52.4	1382	3	US-09-457-040B-7	Sequence 7, Appli
43	43	51.2	13	3	US-09-258-754-216	Sequence 216, App
44	43	51.2	13	3	US-09-042-107-216	Sequence 216, App
45	43	51.2	13	4	US-09-722-250D-216	Sequence 216, App

ALIGNMENTS

RESULT 1

US-09-139-802-2

; Sequence 2, Application US/09139802

; Patent No. 6180084

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing

; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: P-LJ 3203

; CURRENT APPLICATION NUMBER: US/09/139,802

; CURRENT FILING DATE: 1998-08-25

; EARLIER APPLICATION NUMBER: 08/926,914

; EARLIER FILING DATE: 1997-09-10

; EARLIER APPLICATION NUMBER: 08/710,067

; EARLIER FILING DATE: 1996-09-10

; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-139-802-2

Query Match 59.5%; Score 50; DB 3; Length 13;

Best Local Similarity 53.8%; Pred. No. 0.88;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPKVCPRCESNC 13

Db 1 CGRECPRLCQSSC 13

RESULT 2

US-09-659-786-2

; Sequence 2, Application US/09659786

; Patent No. 6491894

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing

; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: P-LJ 3203

; CURRENT APPLICATION NUMBER: US/09/659,786

; CURRENT FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-659-786-2

Query Match 59.5%; Score 50; DB 4; Length 13;
Best Local Similarity 53.8%; Pred. No. 0.88; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 1 CGRCPRLCQSSC 13

RESULT 3
US-08-926-914-2
; Sequence 2, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/926,914
; APPLICATION NUMBER: 10-SEP-1997
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-926-914-2

Query Match 59.5%; Score 50; DB 4; Length 13;
Best Local Similarity 53.8%; Pred. No. 0.88; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 1 CGRCPRLCQSSC 13

RESULT 4
US-09-428-082B-1071
; Sequence 1071, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-428-082B-1071

Query Match 59.5%; Score 50; DB 4; Length 13;
Best Local Similarity 53.8%; Pred. No. 0.88; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 1 CGRCPRLCQSSC 13

RESULT 5
US-09-621-976-6330
; Sequence 6330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6330
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6330

Query Match 57.1%; Score 48; DB 4; Length 98;
Best Local Similarity 53.8%; Pred. No. 9.7; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 2;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 74 CTKPCPPKCPSSC 86

RESULT 6
US-09-270-767-57784
; Sequence 57784, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57784
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57784

Query Match 56.0%; Score 47; DB 4; Length 58;
Best Local Similarity 53.8%; Pred. No. 8.2;
Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 1 CPKVCPRCESNC 13
| :|||||
Db 35 CARICPREPEVC 47

RESULT 7

US-09-270-767-42488
; Sequence 42488, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42488
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42488

Query Match 56.0%; Score 47; DB 4; Length 118;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 1 CPKVCPRCESNC 13
| :|||||
Db 35 CARICPREPEVC 47

RESULT 8

US-08-857-076-105
; Sequence 105, Application US/08857076C
; Patent No. 6225120
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Kowsek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351001
; CURRENT APPLICATION NUMBER: US/08/857,076C
; CURRENT FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-08-857-076-105

Query Match 56.0%; Score 47; DB 3; Length 383;
Best Local Similarity 46.2%; Pred. No. 44;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CPKVCPRCESNC 13
| :|||||
Db 86 CQTKCPEKCRNC 98

RESULT 9

US-08-537-210A-1
; Sequence 1, Application US/08537210A
; Patent No. 5780300
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Teakonas, Spyridon
; APPLICANT: Fortini, Mark
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,210A
; FILING DATE: 29-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1015 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: hum N (Human No. 5780300ch 2)
; LOCATION: 1155...2169
; OTHER INFORMATION: Highly conserved ankyrin repeat
; OTHER INFORMATION: region of No. 5780300ch
US-08-537-210A-1

Query Match 54.8%; Score 46; DB 1; Length 1015;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRCESNC 13
| :|||||
Db 214 CPS--PRDCESGC 224

RESULT 10

US-09-113-825-1
; Sequence 1, Application US/09113825
; Patent No. 6149902
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Teakonas, Spyridon
; APPLICANT: Fortini, Mark
; APPLICANT: Matsuno, Kenji

;; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
 ;; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY

;; NUMBER OF SEQUENCES: 4

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036/2711

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/113,825

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/537,210

;; FILING DATE: 29-SEP-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Mistrock, S. Leslie

;; REGISTRATION NUMBER: 18,872

;; REFERENCE/DOCKET NUMBER: 7326-027

;; TELEPHONE: 212-790-9090

;; TELEFAX: 212-869-8864

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 1015 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: unknown

;; MOLECULE TYPE: protein

;; FEATURE:

;; NAME/KEY: hum N (Human No. 6149902ch 2)

;; LOCATION: 1155...2169

;; OTHER INFORMATION: Highly conserved ankyrin repeat

;; OTHER INFORMATION: region of No. 6149902ch

US-09-113-825-1

Query Match 54.8%; Score 46; DB 3; Length 1015;

Best Local Similarity 61.5%; Pred. No. 1.4e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/185,432

;; FILING DATE: 21-JAN-1994

;; CLASSIFICATION: 530

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Mistrock, S. Leslie

;; REGISTRATION NUMBER: 18,872

;; REFERENCE/DOCKET NUMBER: 7326-006

;; TELEPHONE: (212) 790-9090

;; TELEFAX: (212) 869-8864/9741

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 16:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 2471 amino acids

;; TYPE: amino acid

;; TOPOLOGY: unknown

;; MOLECULE TYPE: protein

US-08-185-432-16

Query Match 54.8%; Score 46; DB 1; Length 2471;

Best Local Similarity 61.5%; Pred. No. 3.1e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPECESNC 13

DB 1368 CPS--PRDCESGC 1378

RESULT 12

US-08-083-590A-19

; Sequence 19, Application US/08083590A

; Patent No. 5786158

; GENERAL INFORMATION:

; APPLICANT: Artavanis-Tsakonas, S. et al.

; TITLE OF INVENTION: Therapeutic And Diagnostic Methods

; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/083,590A

;; FILING DATE: 25-JUN-1993

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Mistrock, S. Leslie

;; REGISTRATION NUMBER: 18,872

;; REFERENCE/DOCKET NUMBER: 7326-015

;; TELEPHONE: 212 790-9090

;; TELEFAX: 212 8698864/9741

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 19:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 2471 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

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; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19

Query Match      54.8%; Score 46; DB 1; Length 2471;
Best Local Similarity 61.5%; Pred. No. 3.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY      1 CPKVCPRCESNC 13
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Db      1368 CPS--PRDCESGC 1378

RESULT 13
US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-19

Query Match      54.8%; Score 46; DB 3; Length 2471;
Best Local Similarity 61.5%; Pred. No. 3.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY      1 CPKVCPRCESNC 13
      |||:|||||
Db      1368 CPS--PRDCESGC 1378

RESULT 14
US-08-899-232-1
; Sequence 1, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
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; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1
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Query Match      54.8%; Score 46; DB 4; Length 2471;
Best Local Similarity 61.5%; Pred. No. 3.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
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QY      1 CPKVCPRCESNC 13
      |||:|||||
Db      1368 CPS--PRDCESGC 1378
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RESULT 15
US-09-121-457-1
; Sequence 1, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-457-1
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Query Match      54.8%; Score 46; DB 4; Length 2471;
Best Local Similarity 61.5%; Pred. No. 3.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
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```
QY      1 CPKVCPRCESNC 13
      |||:|||||
Db      1368 CPS--PRDCESGC 1378
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Search completed: November 16, 2004, 14:32:12
Job time : 19.7296 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:30:02 ; Search time 60.8302 Seconds
(without alignments)
75.615 Million cell updates/sec

Title: US-10-784-537-3

Perfect score: 84

Sequence: 1 CPKVCPRCESNC 13

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Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	53	63.1	844	17	US-10-411-910A-48
3	51	60.7	198	17	US-10-425-115-325327
4	51	60.7	762	15	US-10-282-122A-48817
5	50	59.5	9	16	US-10-363-204-123
6	50	59.5	13	9	US-09-765-086-2
7	50	59.5	13	9	US-09-840-277-32
8	50	59.5	13	14	US-10-264-374-2
9	50	59.5	13	14	US-10-375-992-2
10	50	59.5	13	15	US-10-609-217-1071
11	50	59.5	13	15	US-10-632-388-1071
12	50	59.5	13	15	US-10-651-723-1071
13	50	59.5	13	15	US-10-645-761-1071

14	50	59.5	13	15	US-10-666-696-1071	Sequence 1071, Ap
15	50	59.5	13	15	US-10-653-048-1071	Sequence 1071, Ap
16	50	59.5	13	15	US-10-264-374-2	Sequence 2, Appli
17	50	59.5	13	16	US-10-375-992-2	Sequence 2, Appli
18	50	59.5	1594	16	US-10-408-765A-1155	Sequence 260282,
19	48	57.1	79	17	US-10-425-115-260282	Sequence 1155, Ap
20	48	57.1	121	10	US-09-764-891-4135	Sequence 4135, Ap
21	48	57.1	132	15	US-10-264-237-2213	Sequence 2213, Ap
22	47	56.0	31	16	US-10-363-204-125	Sequence 125, App
23	47	56.0	383	9	US-09-205-658-105	Sequence 105, App
24	47	56.0	383	10	US-09-844-353A-105	Sequence 105, App
25	47	56.0	383	10	US-09-963-693-105	Sequence 52651, A
26	47	56.0	461	15	US-10-282-122A-52367	Sequence 52367, A
27	47	56.0	470	15	US-10-282-122A-52367	Sequence 52, Appli
28	46	54.8	103	9	US-09-950-933A-52	Sequence 304853,
29	46	54.8	236	17	US-10-425-115-304853	Sequence 1, Appli
30	46	54.8	237	17	US-10-425-115-304851	Sequence 2, Appli
31	46	54.8	1015	15	US-10-419-026-1	Sequence 145825,
32	46	54.8	2203	16	US-10-322-281-726	Sequence 58723, A
33	46	54.8	2469	14	US-10-190-115-2	Sequence 5212, A
34	46	54.8	2469	15	US-10-369-072-2	Sequence 293314, A
35	46	54.8	2471	17	US-10-720-896A-12	Sequence 43605, A
36	45	53.6	81	15	US-10-424-599-145825	Sequence 314179,
37	45	53.6	119	16	US-10-767-701-58723	Sequence 291729,
38	45	53.6	145	15	US-10-425-114-51212	Sequence 314175,
39	45	53.6	145	17	US-10-425-115-293314	Sequence 9529, Ap
40	45	53.6	152	16	US-10-767-701-43605	Sequence 208114,
41	45	53.6	235	17	US-10-425-115-314179	
42	45	53.6	249	17	US-10-425-115-291729	
43	45	53.6	260	17	US-10-425-115-314175	
44	45	53.6	344	17	US-10-739-930-9529	
45	45	53.6	349	17	US-10-425-115-208114	

ALIGNMENTS

RESULT 1

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US-10-363-204-127
; Sequence 127, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127

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Query Match 100.0%; Score 84; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13

Db 1 CPKVCPRCESNC 13

RESULT 2

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US-10-411-910A-48
; Sequence 48, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:

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; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Desulfitobacterium hafniense
US-10-411-910A-48

Query Match          63.1%; Score 53; DB 17; Length 844;
Best Local Similarity 53.8%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
DB 177 CGRVCPHSCEAQC 189

RESULT 3
US-10-425-115-325327
; Sequence 325327, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325327
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRA4577_5976C.1.pep
US-10-425-115-325327

Query Match          60.7%; Score 51; DB 17; Length 198;
Best Local Similarity 53.8%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
DB 76 CPKTCFNKCLARC 88

RESULT 4
US-10-282-122A-48817
; Sequence 48817, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
```

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; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48817
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48817

Query Match          60.7%; Score 51; DB 15; Length 762;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRC--CESNC 13
DB 388 CGRVCPRKQCESKC 402

RESULT 5
US-10-363-204-123
; Sequence 123, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-204-123

Query Match          59.5%; Score 50; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CPRECESNC 13
DB 1 CPRECESIC 9
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RESULT 6
 US-09-765-086-2
 ; Sequence 2, Application US/09765086
 ; Patent No. US20010046498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; APPLICANT: Wadih, Arap
 ; APPLICANT: Bredesen, Dale E.
 ; APPLICANT: Ellerby, H. Michael
 ; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides with
 ; TITLE OF INVENTION: Pro-Apoptotic Activity
 ; FILE REFERENCE: P-LJ 3844
 ; CURRENT APPLICATION NUMBER: US/09/765,086
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US 09/489,582
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 235
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-09-765-086-2

Query Match 59.5%; Score 50; DB 9; Length 13;
 Best Local Similarity 53.8%; Pred. No. 4.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;
 Qy 1 CPKVCPRCESNC 13
 | : ||| | : ||
 Db 1 CGRCPRLCQSSC 13

RESULT 7
 US-09-840-277-32
 ; Sequence 32, Application US/09840277
 ; Patent No. US20020168363A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: KOHNO, TADAIKO
 ; APPLICANT: LACEY, DAVID LEE
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
 ; FILE REFERENCE: A-688A
 ; CURRENT APPLICATION NUMBER: US/09/840,277
 ; CURRENT FILING DATE: 2001-08-14
 ; PRIOR APPLICATION NUMBER: 60/198,919
 ; PRIOR FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 60/201,394
 ; PRIOR FILING DATE: 2000-05-03
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Integrin antagonist peptide
 US-09-840-277-32

Query Match 59.5%; Score 50; DB 9; Length 13;
 Best Local Similarity 53.8%; Pred. No. 4.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;
 Qy 1 CPKVCPRCESNC 13
 | : ||| | : ||
 Db 1 CGRCPRLCQSSC 13

RESULT 8
 US-10-264-374-2
 ; Sequence 2, Application US/10264374
 ; Publication No. US20030113320A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
 ; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
 ; TITLE OF INVENTION: Same
 ; FILE REFERENCE: P-LJ 3203
 ; CURRENT APPLICATION NUMBER: US/10/264,374
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: US/09/139,802
 ; PRIOR FILING DATE: 1998-08-25
 ; PRIOR APPLICATION NUMBER: 08/926,914
 ; PRIOR FILING DATE: 1997-09-10
 ; PRIOR APPLICATION NUMBER: 08/710,067
 ; PRIOR FILING DATE: 1996-09-10
 ; NUMBER OF SEQ ID NOS: 226
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-264-374-2

Query Match 59.5%; Score 50; DB 14; Length 13;
 Best Local Similarity 53.8%; Pred. No. 4.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;
 Qy 1 CPKVCPRCESNC 13
 | : ||| | : ||
 Db 1 CGRCPRLCQSSC 13

RESULT 9
 US-10-375-992-2
 ; Sequence 2, Application US/10375992
 ; Publication No. US20030152578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
 ; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
 ; NUMBER OF SEQUENCES: 199
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/375,992
 ; FILING DATE: 27-Feb-2003
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/926,914
 ; FILING DATE: 10-SEP-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 2725

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-375-992-2

Query Match 59.5%; Score 50; DB 14; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPKVCPRCESNC 13
| : ||| | : ||
Db 1 CGRECPRLCQSC 13

RESULT 10
US-10-609-217-1071
; Sequence 1071, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-1071

Query Match 59.5%; Score 50; DB 15; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPKVCPRCESNC 13
| : ||| | : ||
Db 1 CGRECPRLCQSC 13

RESULT 11
US-10-632-388-1071
; Sequence 1071, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-1071

Query Match 59.5%; Score 50; DB 15; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPKVCPRCESNC 13
| : ||| | : ||
Db 1 CGRECPRLCQSC 13

RESULT 12
US-10-651-723-1071
; Sequence 1071, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-651-723-1071

Query Match 59.5%; Score 50; DB 15; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPKVCPRCESNC 13
| : ||| | : ||
Db 1 CGRECPRLCQSC 13

RESULT 13
US-10-645-761-1071
; Sequence 1071, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-1071

Query Match 59.5%; Score 50; DB 15; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 1 CGRECPRLCQSSC 13

RESULT 14

US-10-666-696-1071
; Sequence 1071, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-666-696-1071

Query Match 59.5%; Score 50; DB 15; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 1 CGRECPRLCQSSC 13

RESULT 15

US-10-653-048-1071
; Sequence 1071, Application US/10653048
; Publication No. US2004008778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-653-048-1071

Query Match 59.5%; Score 50; DB 15; Length 13;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
| : ||| | : |
Db 1 CGRECPRLCQSSC 13

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Job time : 69.8302 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:19:17 ; Search time 212.17 Seconds
(without alignments)
67.889 Million cell updates/sec

Title: US-10-784-537-3

Perfect score: 84

Sequence: 1 CPKVCPRCESNC 13

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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33: /cgn2_6/ptodata/1/paa/US107 COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
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2	84	100.0	13	1	PCT-US02-27836-60	Sequence 60, Appl
3	84	100.0	13	29	US-10-363-204-127	Sequence 127, App
4	84	100.0	13	33	US-10-784-537-3	Sequence 3, Appli
5	68.5	81.5	12	33	US-10-784-537-8	Sequence 8, Appli
6	55	65.5	500	36	US-60-581-351-5704	Sequence 5704, Ap
7	53	63.1	464	36	US-60-581-351-5582	Sequence 5582, Ap
8	53	63.1	466	36	US-60-581-351-5583	Sequence 5583, Ap
9	53	63.1	649	36	US-60-581-351-5898	Sequence 5898, Ap
10	53	63.1	672	36	US-60-581-351-5795	Sequence 5795, Ap
11	53	63.1	844	30	US-10-411-910A-48	Sequence 48, Appl
12	53	63.1	844	33	US-10-763-712A-48	Sequence 48, Appl
13	52	61.9	413	22	US-09-791-537-92086	Sequence 92086, A
14	52	61.9	413	36	US-60-581-351-5573	Sequence 5573, Ap
15	51	60.7	198	30	US-10-425-115-325327	Sequence 325327, A
16	51	60.7	488	22	US-09-791-537-92102	Sequence 92102, A
17	51	60.7	468	36	US-60-581-351-5784	Sequence 5784, Ap
18	51	60.7	763	28	US-10-282-122A-48817	Sequence 48817, A
19	51	60.7	763	19	US-09-540-209B-8497	Sequence 8497, Ap
20	51	60.7	763	36	US-60-581-351-5770	Sequence 5770, Ap
21	50	59.5	8	33	US-10-784-537-6	Sequence 6, Appli
22	50	59.5	9	1	PCT-US01-27692A-123	Sequence 123, App
23	50	59.5	9	1	PCT-US02-27836-56	Sequence 56, Appl
24	50	59.5	24	29	US-10-363-204-123	Sequence 123, App
25	50	59.5	25	50	US-10-784-537-2	Sequence 2, Appli
26	50	59.5	13	1	PCT-US00-01602-2	Sequence 2, Appli
27	50	59.5	13	1	PCT-US99-25044-1027	Sequence 1027, Ap
28	50	59.5	13	1	PCT-US99-25044-1071	Sequence 1071, Ap
29	50	59.5	13	11	US-08-710-067-5	Sequence 5, Appli
30	50	59.5	13	16	US-09-235-903-2	Sequence 2, Appli
31	50	59.5	13	18	US-09-489-582-2	Sequence 2, Appli
32	50	59.5	13	19	US-09-563-286B-1071	Sequence 1071, Ap
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34	50	59.5	13	22	US-09-765-086-2	Sequence 2, Appli
35	50	59.5	13	23	US-09-840-277B-32	Sequence 32, Appl
36	50	59.5	13	23	US-09-840-277B-32	Sequence 32, Appl
37	50	59.5	13	28	US-10-264-374-2	Sequence 2, Appli
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44	50	59.5	13	32	US-10-666-696-1071	Sequence 1071, Ap
45	50	59.5	45	36	US-60-143-992-1206	Sequence 1206, Ap

ALIGNMENTS

RESULT 1
PCT-US01-27692A-127
; Sequence 127, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-127

Query Match 100.0%; Score 84; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPCESNC 13
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DB 1 CPKVCPCESNC 13

RESULT 2
PCT-US02-27836-60
; Sequence 60, Application PC/TUS0227836
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System (applicant for the
; APPLICANT: purposes of all designated states except US)
; APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of
; APPLICANT: America only)
; APPLICANT: Arap, Wadih (applicant for the purpose of the United States of
; APPLICANT: only)
; APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of
; APPLICANT: America only)
; TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
; FILE REFERENCE: 5774.P009PCT
; CURRENT APPLICATION NUMBER: PCT/US02/27836
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US02-27836-60

Query Match 100.0%; Score 84; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPCESNC 13
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DB 1 CPKVCPCESNC 13

RESULT 3
US-10-363-204-127
; Sequence 127, Application US/10363204
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127

Query Match 100.0%; Score 84; DB 29; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPCESNC 13
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DB 1 CPKVCPCESNC 13

RESULT 4
US-10-784-537-3
; Sequence 3, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-784-537-3

Query Match 100.0%; Score 84; DB 33; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPKVCPCESNC 13
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DB 1 CPKVCPCESNC 13

RESULT 5
US-10-784-537-8
; Sequence 8, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-784-537-8

Query Match      81.5%; Score 68.5; DB 33; Length 12;
Best Local Similarity 92.3%; Pred. No. 0.024;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 CPKVCPRCESNC 13
      | : ||| : |||
Db      1 CPKVCPRC-SNC 12

RESULT 6
US-60-581-351-5704
; Sequence 5704, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5704
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Clostridium thermocellum ATCC 27405
US-60-581-351-5704

Query Match      65.5%; Score 55; DB 36; Length 500;
Best Local Similarity 61.5%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 13
      | : ||| : |||
Db      159 CGRVCPHTCESQC 171

RESULT 7
US-60-581-351-5582
; Sequence 5582, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5582
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Thermoanaerobacter tengcongensis
US-60-581-351-5582

Query Match      63.1%; Score 53; DB 36; Length 464;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY      1 CPKVCPRC--CESNC 13
      | : ||| : |||
Db      87 CGRVCPQEQCEKNC 101

RESULT 8
US-60-581-351-5583
; Sequence 5583, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5583
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Thermoanaerobacter tengcongensis
US-60-581-351-5583

Query Match      63.1%; Score 53; DB 36; Length 466;
Best Local Similarity 60.0%; Pred. No. 90;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY      1 CPKVCPRC--CESNC 13
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Db      90 CGRVCPQEQCEKNC 104

RESULT 9
US-60-581-351-5898
; Sequence 5898, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5898
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Wolinella succinogenes
US-60-581-351-5898

Query Match      63.1%; Score 53; DB 36; Length 649;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 13
      | : ||| : |||
Db      194 CGRVCPHPCESAC 206

RESULT 10
US-60-581-351-5795
; Sequence 5795, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5795
; LENGTH: 672
; TYPE: PRT
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; ORGANISM: Geobacter metallireducens
US-60-581-351-5795

Query Match      63.1%; Score 53; DB 36; Length 672;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CPKVCPRECESNC 13
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Db      203 CGRVCPHCPTC 215

RESULT 11
US-10-411-910A-48
; Sequence 48, Application US/10411910A
; GENERAL INFORMATION:
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Desulfotobacterium hafniense
US-10-411-910A-48

Query Match      63.1%; Score 53; DB 30; Length 844;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CPKVCPRECESNC 13
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Db      177 CGRVCPHSCQAQC 189

RESULT 12
US-10-763-712A-48
; Sequence 48, Application US/10763712A
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; TITLE OF INVENTION: Production
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Desulfotobacterium hafniense
US-10-763-712A-48

Query Match      63.1%; Score 53; DB 33; Length 844;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CPKVCPRECESNC 13
       |:|:|:| |:|:|
Db      177 CGRVCPHSCQAQC 189

RESULT 13
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US-09-791-537-92086
; Sequence 92086, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92086
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-09-791-537-92086

Query Match      61.9%; Score 52; DB 22; Length 413;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy      1 CPKVCP--RECESNC 13
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Db      33 CGRICPQDRKCEGNC 47

RESULT 14
US-60-581-351-5573
; Sequence 5573, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5573
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-60-581-351-5573

Query Match      61.9%; Score 52; DB 36; Length 413;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy      1 CPKVCP--RECESNC 13
       |:|:|:| |:|:|
Db      33 CGRICPQDRKCEGNC 47

RESULT 15
US-10-425-115-325327
; Sequence 325327, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325327
; LENGTH: 198
; TYPE: PRT
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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5976C.1.pep
US-10-425-115-325327

Query Match 60.7%; Score 51; DB 30; Length 198;
Best Local Similarity 53.8%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CPKVCPECESNC 13
Db 76 CPKTCPNKCLAF 88

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OM protein - protein search, using sw model

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Title: US-10-784-537-1

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6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	31	6 US-10-489-071-58	Sequence 58, Appl
2	67.5	34.1	895	6 US-10-732-923-15015	Sequence 15015, A
3	66	33.3	35823	6 US-10-874-049-1	Sequence 1, Appli
4	65.5	33.1	35346	6 US-10-874-049-2	Sequence 2, Appli
5	58.5	29.5	143	6 US-10-220-366A-18045	Sequence 18045, A
6	56.5	28.5	1602	1 PCT-US04-33017-4	Sequence 4, Appli
7	56.5	28.5	1602	6 US-10-962-128-4	Sequence 4, Appli
8	56	28.3	123	6 US-10-220-366A-15841	Sequence 15841, A
9	55	27.8	119	6 US-10-220-366A-14903	Sequence 14903, A
10	54.5	27.5	945	6 US-10-955-952-146	Sequence 146, App
11	54.5	27.5	945	6 US-10-157-779-146	Sequence 146, App
12	54.5	27.5	945	6 US-10-964-241-146	Sequence 146, App
13	54.5	27.5	945	6 US-10-972-024-292	Sequence 292, App
14	54.5	27.5	994	6 US-10-732-923-14191	Sequence 14191, A
15	54.5	27.5	1077	6 US-10-732-923-14210	Sequence 14210, A
16	54.5	27.5	3654	6 US-10-732-923-20601	Sequence 20601, A
17	53.5	27.0	245	6 US-10-732-923-14190	Sequence 14190, A
18	53.5	27.0	1184	6 US-10-153-604B--89	Sequence 89, Appl
19	53.5	27.0	2055	6 US-10-481-582-3	Sequence 3, Appli
20	53.5	27.0	2497	6 US-10-481-582-4	Sequence 4, Appli
21	53	26.8	1418	6 US-10-732-923-13624	Sequence 13624, A
22	52.5	26.5	832	6 US-10-512-109-29	Sequence 29, Appl
23	52	26.3	33	6 US-10-966-673-75	Sequence 75, Appl
24	52	26.3	146	6 US-10-399-103A-851	Sequence 851, App
25	52	26.3	786	6 US-10-874-049-3	Sequence 3, Appli

26	51.5	26.0	70	6 US-10-894-314A-244	Sequence 244, App
27	51.5	26.0	70	6 US-10-894-314A-256	Sequence 256, App
28	51.5	26.0	123	6 US-10-363-374-14	Sequence 14, Appl
29	51.5	26.0	145	6 US-10-220-366A-16237	Sequence 834, App
30	51.5	26.0	199	6 US-10-399-103A-834	Sequence 834, App
31	51.5	26.0	461	6 US-10-965-357-4	Sequence 4, Appli
32	51.5	26.0	461	6 US-10-965-357-6	Sequence 6, Appli
33	51.5	26.0	461	6 US-10-965-357-28	Sequence 28, Appl
34	51.5	26.0	461	6 US-10-967-851-4	Sequence 4, Appli
35	51.5	26.0	461	6 US-10-967-851-6	Sequence 28, Appl
36	51.5	26.0	461	6 US-10-967-851-28	Sequence 1061, Ap
37	50.5	25.5	26	6 US-10-915-740A-1061	Sequence 15949, A
38	50.5	25.5	74	6 US-10-220-366A-15949	Sequence 15949, A
39	50.5	25.5	120	6 US-10-220-366A-14519	Sequence 14519, A
40	50.5	25.5	671	6 US-10-841-250-6	Sequence 6, Appli
41	50	25.3	111	6 US-10-220-366A-15700	Sequence 15700, A
42	50	25.3	116	6 US-10-220-366A-15951	Sequence 15951, A
43	50	25.3	129	6 US-10-220-366A-27094	Sequence 27094, A
44	50	25.3	744	6 US-10-732-923-14192	Sequence 14192, A
45	50	25.3	779	6 US-10-967-702-119	Sequence 119, App

ALIGNMENTS

RESULT 1
US-10-489-071-58
; Sequence 58, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUALINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-58

Query Match 100.0%; Score 198; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.4e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31
Db 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31

RESULT 2
US-10-732-923-15015
; Sequence 15015, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 15015
; TYPE: PRT
; LENGTH: 895
; ORGANISM: Oryza sativa (indica cultivar-group)
US-10-732-923-15015

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Query Match      34.1%; Score 67.5; DB 6; Length 895;
Best Local Similarity 45.7%; Pred. No. 3.1;
Matches 16; Conservative 3; Mismatches 9; Indels 7; Gaps 3;

QY 2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
DB 647 YNPC--GQQMCGKDKACVNGTTCCKYCGGSKSC 679

RESULT 3
US-10-874-049-1
; Sequence 1, Application US/10874049
; GENERAL INFORMATION:
; APPLICANT: Shen, Jerry Yuiqiao
; APPLICANT: Shen, Annie
; APPLICANT: Perez, Aleida
; APPLICANT: Sevilla, Elizabeth
; APPLICANT: Aspelund, Amy
; TITLE OF INVENTION: Subgroup B Adenovirus Vectors for Treating Disease
; FILE REFERENCE: ONYX 1053-ORD
; CURRENT APPLICATION NUMBER: US/10/874,049
; CURRENT FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/488678
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 35823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-874-049-1

Query Match      33.3%; Score 66; DB 6; Length 35823;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTWCADGCSRSC 31
DB 14755 CGTCAGCTGAGACCATCATGCGACAC 14781

RESULT 4
US-10-874-049-2
; Sequence 2, Application US/10874049
; GENERAL INFORMATION:
; APPLICANT: Shen, Jerry Yuiqiao
; APPLICANT: Shen, Annie
; APPLICANT: Perez, Aleida
; APPLICANT: Sevilla, Elizabeth
; APPLICANT: Aspelund, Amy
; TITLE OF INVENTION: Subgroup B Adenovirus Vectors for Treating Disease
; FILE REFERENCE: ONYX 1053-ORD
; CURRENT APPLICATION NUMBER: US/10/874,049
; CURRENT FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/488678
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 35346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-874-049-2

Query Match      33.1%; Score 65.5; DB 6; Length 35346;
Best Local Similarity 39.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 5 CIRECESICGADGAC--WTWCADGCSRSC 31
DB 30478 CCAACAACGGTGGTCACTTCTTGCTGC 30505

Query Match      34.1%; Score 67.5; DB 6; Length 895;
Best Local Similarity 45.7%; Pred. No. 3.1;
Matches 16; Conservative 3; Mismatches 9; Indels 7; Gaps 3;

QY 2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
DB 647 YNPC--GQQMCGKDKACVNGTTCCKYCGGSKSC 679

RESULT 5
US-10-220-366A-18045
; Sequence 18045, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 18045
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(143)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-18045

Query Match      29.5%; Score 58.5; DB 6; Length 143;
Best Local Similarity 35.5%; Pred. No. 5.2;
Matches 11; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

QY 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
DB 4 CVRXCAWCVXMCQ-ERLC--WCVGSCNRVC 31

RESULT 6
PCT-US04-33017-4
; Sequence 4, Application PC/TUS0433017
; GENERAL INFORMATION:
; APPLICANT: University of Massachusetts
; APPLICANT: LAMBERT, David G.
; APPLICANT: CZECH, Michael P.
; APPLICANT: CRONIN, Thomas
; TITLE OF INVENTION: VARIANT POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: FLEKSTRIN HOMOLOGY DOMAINS AND USES THEREFOR
; FILE REFERENCE: UMY-086PC
; CURRENT APPLICATION NUMBER: PCT/US04/33017
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: 60/509777
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1602
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-33017-4

Query Match      28.5%; Score 56.5; DB 1; Length 1602;
Best Local Similarity 45.8%; Pred. No. 70;
Matches 11; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 5 CIRECESICGADGACWTWCADGCS 28
DB 715 CTGCTCTCGCGTCAT-CATGCT 737

RESULT 7
US-10-962-128-4
; Sequence 4, Application US/10962128
; GENERAL INFORMATION:
; APPLICANT: LAMBERT, David G.
; APPLICANT: CZECH, Michael P.
```

```
; APPLICANT: CRONIN, Thomas
; TITLE OF INVENTION: VARIANT POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: PLEKSTRIN HOMOLOG DOMAIN AND USES THEREFOR
; FILE REFERENCE: UMY-086
; CURRENT APPLICATION NUMBER: US/10/962,128
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: 60/509777
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1602
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-962-128-4

Query Match      28.5%; Score 56.5; DB 6; Length 1602;
Best Local Similarity 45.8%; Pred. No. 70;
Matches 11; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Qy 5 CIRECESICGADGACWTWCADGCS 28
Db 715 CTGTCCTTCCGCGTCAT-CATGCT 737

RESULT 8
US-10-220-366A-15841
; Sequence 15841, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 15841
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(123)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-15841

Query Match      28.3%; Score 56; DB 6; Length 123;
Best Local Similarity 29.0%; Pred. No. 8.2;
Matches 9; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
Db 59 CVSTCVCPVPVCTCDVCMSACVCTCLVC 89

RESULT 9
US-10-220-366A-14903
; Sequence 14903, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
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; SOFTWARE: Custom
; SEQ ID NO 14903
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(119)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-14903

Query Match      27.8%; Score 55; DB 6; Length 119;
Best Local Similarity 37.0%; Pred. No. 10;
Matches 10; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

Qy 5 CIRECESICGADGACWTWCADGCSRSC 31
Db 94 CVRVCAVC--SGACGCTCVTXMSLAC 118

RESULT 10
US-10-955-952-146
; Sequence 146, Application US/10955952
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C12
; CURRENT APPLICATION NUMBER: US/10/955,952
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: US/10/121,058
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 146
; LENGTH: 945
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-955-952-146
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; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,783
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/728,628
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/783,066
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/816,828
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 584
; SOFTWARE: Custom
; SEQ ID NO 292
; LENGTH: 945
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-024-292

Query Match      27.5%; Score 54.5; DB 6; Length 945;
Best Local Similarity 40.6%; Pred. No. 70;
Matches 13; Conservative 1; Mismatches 9; Indels 9; Gaps 1;

QY      9 CBSICGADG-----ACWTWCADGCGSRSC 31
Db      295 CTTICPDGANTWENKWSACSTECARHSREC 326

RESULT 14
US-10-732-923-14191
; Sequence 14191, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 14191
; LENGTH: 994
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-14191

Query Match      27.5%; Score 54.5; DB 6; Length 994;
Best Local Similarity 32.5%; Pred. No. 73;
Matches 13; Conservative 4; Mismatches 12; Indels 11; Gaps 3;

QY      1 CYN-LCIRECESICGADG-----CWTWCADGCGSR 30
Db      375 CQHTCTCKHKVTEVDGCPGRHKAGPEC-LQCEEGCKSK 413

RESULT 15
US-10-732-923-14210
; Sequence 14210, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 14210
; LENGTH: 1077

; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-732-923-14210

Query Match      27.5%; Score 54.5; DB 6; Length 1077;
Best Local Similarity 30.6%; Pred. No. 79;
Matches 11; Conservative 3; Mismatches 15; Indels 7; Gaps 1;

QY      1 CYNLC-----IRECESICGADGACWTWCADGCSR 29
Db      698 CGELCNKLLSCKTHFCCKLCHPDGCESSCKKCGK 733

Search completed: November 16, 2004, 14:47:12
Job time : 15.0377 secs
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:15:03 ; Search time 35.0943 Seconds
(without alignments)
84.991 Million cell updates/sec

Title: US-10-784-537-1
Perfect score: 198
Sequence: 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	36.4	654	2 T30136	hypothetical prote
2	69.5	35.1	662	2 T32271	hypothetical prote
3	67	33.8	61	2 B34123	depressant insect
4	65.5	33.1	3133	2 S52093	hemocytin - silkw
5	64	32.3	85	2 A51616	depressant insect
6	64	32.3	1513	2 T23681	hypothetical prote
7	63.5	32.1	294	2 T23682	hypothetical prote
8	62.5	31.6	163	2 T22099	hypothetical prote
9	62.5	31.6	163	2 T22100	hypothetical prote
10	62.5	31.6	164	2 T22102	hypothetical prote
11	61.5	31.1	124	2 A21761	high-cysteine chor
12	60.5	30.6	728	2 T20561	hypothetical prote
13	60	30.3	372	2 T23680	hypothetical prote
14	59.5	30.1	314	2 T27686	hypothetical prote
15	59.5	30.1	856	2 T52415	polycomb protein E
16	59.5	30.1	898	2 T01503	hypothetical prote
17	59.5	30.1	2150	2 T32497	hypothetical prote
18	59	29.8	85	2 A40472	depressant insect
19	59	29.8	103	2 T20283	hypothetical prote
20	59	29.8	328	2 G89152	protein C24B5.5 [i
21	58.5	29.5	223	2 B38346	ultra-high-sulfur
22	58.5	29.5	230	2 A38346	ultra-high-sulfur
23	58.5	29.5	295	2 JC5559	lectin-B - Virgini
24	57.5	29.0	74	2 S51533	probable proteinas
25	57.5	29.0	105	2 S23061	chorion protein -
26	57	28.8	258	2 C86541	CT105 hypothetical
27	57	28.8	258	2 D72082	hypothetical prote
28	57	28.8	330	2 T25169	hypothetical prote
29	57	28.8	1133	1 EGRT	epidermal growth f

30	57	28.8	2120	2 T30243	alpha tectorin - c
31	56.5	28.5	61	2 A59352	depressant insect-
32	56.5	28.5	61	2 B59352	depressant insect-
33	56.5	28.5	310	2 JB0394	regulator protein
34	56.5	28.5	1700	2 S08167	balbiani ring 3 pr
35	56.5	28.5	2476	2 T34022	zonadhesin - pig
36	56.5	28.5	2813	1 VMHU	von Willebrand fac
37	56	28.3	61	2 C59352	depressant insect-
38	56	28.3	534	2 T35190	hypothetical prote
39	55.5	28.0	358	2 T23802	hypothetical prote
40	55	27.8	61	2 A59006	excitatory insect
41	55	27.8	83	1 NTSRI2	neurotoxin I' prec
42	55	27.8	272	2 T36770	probable expressio
43	55	27.8	388	2 A88949	protein R09B5.5 [i
44	55	27.8	572	2 T29880	hypothetical prote
45	55	27.8	1390	2 T30346	insulin receptor -

ALIGNMENTS

RESULT 1

T30136
hypothetical protein C14C11.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30136
R:Du, Z.; Gattung, S.
Submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid C14C11.
A:Reference number: Z20742
A:Accession: T30136
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-654 <DUZ>
A:Cross-references: UNIPROT:Q17982; EMBL:U53141; PIDN:AAA96110.1; GSPDB:GN00023; CESP:C14C11.8
A:Experimental source: strain Bristol N2; clone C14C11
C:Genetics:
A:Gene: CESP:C14C11.8
A:Map position: 5
A:Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3

Query Match 36.4%; Score 72; DB 2; Length 654;
Best Local Similarity 32.3%; Pred. No. 1.1;
Matches 10; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
DB 534 CVQACQPQCQQTCCGSNNVCVSACQNSCQSC 564

RESULT 2

T32271
hypothetical protein K03D10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32271
R:White, S.
Submitted to the EMBL Data Library, November 1996
A:Reference number: Z19719
A:Accession: T32271
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-662 <WIL>
A:Cross-references: UNIPROT:O62299; EMBL:Z81561; PIDN:CAB04551.1; GSPDB:GN00019; CESP:C14C11.8
A:Experimental source: clone K03D10
C:Genetics:
A:Gene: CESP:K03D10.1
A:Map position: 1
A:Introns: 23/3; 78/3; 264/3; 597/3
Query Match 35.1%; Score 69.5; DB 2; Length 662;
Best Local Similarity 44.4%; Pred. No. 2;


```

Query Match          33.1%; Score 65.5; DB 2; Length 3133;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 14; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY      2 YNLRCESICGADGACWTWCADGCSRSC 31
      || :||| | | | | | | | | | |
DB      31 YN-VKECELSC-TGQQYTVCADSLRC 57

RESULT 5
A61616
depressant insect toxin LqhIIT2 precursor - scorpion (Leiurus quinquestriatus)
C:Species: Leiurus quinquestriatus hebraeus
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C:Accession: A61616; A34123; A38526
R:Zilberberg, N.; Zlotkin, E.; Gurevitz, M.
Insect Biochem. Mol. Biol. 22, 199-203, 1992
A:Title: Molecular analysis of cDNA and the transcript encoding the depressant
A:Reference number: A61616
A:Accession: A61616
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-85 <ZIL>
A:Cross-references: UNIPROT:Q26292
R:Zlotkin, E.; Fowler, E.; Bitan, M.; Moyer, M.; Adams, M.E.
Toxicol 28, 170, 1990
A:Title: On the chemistry and action of the depressant insect toxins.
A:Reference number: A34123
A:Accession: A34123
A:Molecule type: protein
A:Residues: 22-82 <ZLOI>
R:Zlotkin, E.; Bitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhardt, W.;
Biochemistry 30, 4814-4821, 1991
A:Title: Functional duality and structural uniqueness of depressant insect-selective
A:Reference number: A38526; MUID:91230120; PMID:2029523
A:Accession: A38526
A:Molecule type: protein
A:Residues: 22-82 <ZLO2>
A:Cross-references: CAS:130300-64-0
C:Superfamily: scorpion neurotoxin
C:Keywords: amidated carboxyl end; neurotoxin; venom
F:1-11/Domain: signal sequence #status predicted <SIG>
F:12-21/Domain: propeptide #status predicted <PRO>
F:22-82/Product: depressant insect toxin LqhIIT2 #status experimental <NAT>
F:31-81,35-56,42-63,46-65/Disulfide bonds: #status predicted
F:82/Modified site: amidated carboxyl end (Gly) (amide in mature form from foll

Query Match          32.3%; Score 64; DB 2; Length 85;
Best Local Similarity 50.0%; Pred. No. 1;9;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      5 CIRECESICGADGACWTW 22
      || :||| | | | | | |
DB      42 CDKECKAYGGSYGYCMTW 59

RESULT 6
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23681
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19781
A:Accession: T23681
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1513 <WIL>
A:Cross-references: UNIPROT:O17970; EMBL:Z81573; PIDN:CA804625.1; GSPDB:GN00020
A:Experimental source: clone M02G9
C:Genetics:
A:Gene: CESP:M02G9.1

```

hypothetical protein F42F12.6 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22100
R/Lloyd, C.
submitted to the EMBL Data Library, November 1995
A/Reference number: Z19514
A/Accession: T22100
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-163 <WIL>
A/Cross-references: UNIPROT:Q20343; EMBL:Z68116; PIDN:CAA92172.1; GSPDB:GN00028; CESP:F42F12
A/Experimental source: clone F42F12
C/Genetics:
A/Gene: CESP:F42F12.6
A/Map position: X
A/Introns: 63/3
C/Superfamily: *Caenorhabditis elegans* hypothetical protein F42F12.1

Query Match 31.6%; Score 62.5; DB 2; Length 163;
Best Local Similarity 41.9%; Pred. No. 4.4;
Matches 13; Conservative 4; Mismatches 9; Indels 5; Gaps 2;

QY 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31
|||||:|::|||:| | |
DB 115 CYNLCVHNCAAV--YDGSCTT---DPDFRCC 140

RESULT 10
T22102
hypothetical protein F42F12.1 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22102
R/Lloyd, C.
submitted to the EMBL Data Library, November 1995
A/Reference number: Z19514
A/Accession: T22102
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-164 <WIL>
A/Cross-references: UNIPROT:Q20345; EMBL:Z68116; PIDN:CAA92174.1; GSPDB:GN00028; CESP:F42F12
A/Experimental source: clone F42F12
C/Genetics:
A/Gene: CESP:F42F12.1
A/Map position: X
A/Introns: 64/3
C/Superfamily: *Caenorhabditis elegans* hypothetical protein F42F12.1

Query Match 31.6%; Score 62.5; DB 2; Length 164;
Best Local Similarity 41.9%; Pred. No. 4.4;
Matches 13; Conservative 4; Mismatches 9; Indels 5; Gaps 2;

QY 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31
|||||:|::|||:| | |
DB 116 CYNLCVHNCAAV--YDGSCTT---DPDFRCC 141

RESULT 11
A21761
high-cysteine chorion A 12 protein precursor - silkworm
C/Species: *Bombyx mori* (silkworm)
C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 26-Aug-1999
C/Accession: A21761
R/Itatrou, K.; Tsatilou, S.G.; Kafatos, F.C.
Proc. Natl. Acad. Sci. U.S.A. 81, 4452-4456, 1984
A/Title: DNA sequence transfer between two high-cysteine chorion gene families in the silkworm
A/Reference number: A21761; MUID:84272653; PMID:6589605
A/Accession: A21761
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-124 <IAT>
C/Superfamily: chorion class A protein pc292

```

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27686
R;Thomas, K.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20404
A;Accession: T27686
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-314 <WIL>
A;Cross-references: UNIPROT:Q23390; EMBL:Z70038; PIDN:CAA93886.1; GSPDB:GN00020
A;Experimental source: clone ZK1067
C;Genetics:
A;Gene: CESP:ZK1067.7
A;Map position: 2
A;Introns: 30/3; 296/2
C;Superfamily: gliadin

Query Match      30.1%; Score 59.5; DB 2; Length 314;
Best Local Similarity 29.0%; Pred. No. 15;
Matches      9; Conservative      7; Mismatches      14; Indels      1; Gaps      1;

Qy      1 CYNLCITRECISICGADGACWTWCADGCSRSC 31
      | : : : : | | | | : : |
Db      61 CIPVCIQQQSSC-QTSQCITQQCPACNQQC 90

RESULT 15
T52415
polycomb protein EZAI [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52415
R;Blodeau, P.; Luo, M.; Dennis, E.S.; Peacock, W.J.; Chaudhury, A.M.
submitted to the EMBL data Library, October 1998
A;Reference number: Z26069
A;Accession: T52415
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-856 <BIL>
A;Cross-references: UNIPROT:Q9ZSM8; EMBL:AF100163; PIDN:AAD09108.1

Query Match      30.1%; Score 59.5; DB 2; Length 856;
Best Local Similarity 46.4%; Pred. No. 29;
Matches      13; Conservative      3; Mismatches      7; Indels      5; Gaps      2;

Qy      9 CESTCGADGACWT--WCAD---GCSRSC 31
      | : | : | | | : | : | : |
Db     613 CLSWGCKDCPCLTNETCCEKYCGCSRSC 640

Search completed: November 16, 2004, 14:30:50
Job time : 37.0943 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:14:16 ; Search time 184.83 Seconds
(without alignments)
96.503 Million cell updates/sec

Title: US-10-784-537-1

Perfect score: 198

Sequence: 1 CYNLCRECSICGAGCWTWCADGCSRSC 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	36.4	572	Q17982	Q17982 caenorhabdi
2	69.5	35.1	700	O62299	O62299 caenorhabdi
3	69.5	35.1	700	O8WS94	O8WS94 caenorhabdi
4	69.5	35.1	700	CAB04551	CAB04551 caenorhab
5	69.5	35.1	700	CAE48500	CAE48500 caenorhab
6	67.5	34.1	895	E23 MAIZE	Q884p4 zea mays (m
7	67.5	34.1	895	Q84UI6	Q84ui6 oryza sativ
8	67.5	34.1	895	Q8LLD6	Q8llld6 oryza sativ
9	67	33.8	82	SIX2 LEIOU	P19855 leiurus qui
10	65.5	33.1	3133	HNCT_BOMMO	P98092 bombyx mori
11	65	32.8	89	LCK1_ARATH	P82716 arabidopsis
12	65	32.8	101	Q8BRCS	Q8brcs mus musculu
13	65	32.8	838	Q7UNP4	Q7unp4 rhodopirell
14	64.5	32.6	591	Q6NP04	Q6np04 drosophila
15	64.5	32.6	591	Q6NP04	Q6np04 drosophila
16	64.5	32.6	2174	Q9GQRO	Aar82794 drosophil
17	64.5	32.6	2772	Q9VAV4	Q9vav4 drosophila
18	64.5	32.6	2776	Q869A0	Q869a0 drosophila
19	64.5	32.6	2894	Q7KRX2	Q7kxr2 drosophila
20	64.5	32.6	2894	AAF56795	Aaf56795 drosophil
21	64.5	32.6	2898	Q86829	Q86829 drosophila
22	64	32.3	61	SIX2_BUTAR	P80962 buthacus ar
23	64	32.3	61	SIX4_BUTOC	P55903 buthus occi
24	64	32.3	61	SIX5_BUTOC	P55904 buthus occi
25	64	32.3	85	SIX2_LEIOH	Q26292 leiurus qui
26	64	32.3	1513	Q17970	Q17970 caenorhabdi
27	64	32.3	1630	Q8ILM9	Q8ilm9 plasmodium
28	63.5	32.1	294	Q9XUS0	Q9xus0 caenorhabdi
29	62.5	31.6	49	Q23947	Q23947 drosophila
30	62.5	31.6	49	Q23948	Q23948 drosophila
31	62.5	31.6	101	Q20342	Q20342 caenorhabdi

32	62.5	31.6	101	2	Q20345	Q20345 caenorhabdi
33	62.5	31.6	101	2	Q8I4J0	Q8i4j0 caenorhabdi
34	62.5	31.6	101	2	Q8I4J1	Q8i4j1 caenorhabdi
35	62.5	31.6	101	2	Q8WQ66	Q8wq66 caenorhabdi
36	62.5	31.6	163	2	Q20343	Q20343 caenorhabdi
37	62.5	31.6	231	1	WFD3_HUMAN	Q8iub2 homo sapien
38	62.5	31.6	311	2	Q8RI68	Q8ril68 mus musculu
39	62.5	31.6	476	2	Q8RIH9	Q8rilh9 mus musculu
40	62.5	31.6	493	2	Q7TNG6	Q7tng6 mus musculu
41	62.5	31.6	592	2	Q7R630	Q7r630 giardia lam
42	62.5	31.6	592	2	Q6IS34	Q6is34 mus musculu
43	62.5	31.6	592	2	AAH69956	Aah69956 mus muscu
44	62.5	31.6	657	2	Q8R0K8	Q8r0k8 mus musculu
45	62.5	31.6	1205	2	Q8K0P6	Q8k0p6 mus musculu

ALIGNMENTS

RESULT 1
Q17982 PRELIMINARY; PRT; 572 AA.
AC Q17982;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Prion-like- (Q/N-rich)-domain-bearing protein 13.
GN Name=pqn-13;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Felodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Gattung S.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53141; AAA96110.3; -.
DR PIR; T30136; T30136.
DR HSP; P56679; IPI.
DR WormPep; C14C11.8; CE27684.
DR InterPro; IPR003341; DUF139.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF02363; C.tripleX; 15.
DR PROSITE; PS01186; EGF_2; 1.
KW Prion.
SQ SEQUENCE 572 AA; 60645 MW; 4939A142ABF79C6E CRC64;
Query Match 36.4%; Score 72; DB 2; Length 572;
Best Local Similarity 32.3%; Pred. No. 1.6;

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Matches 10; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
    |||::|||::|||::|||::|||
Db 452 CVQACQPCQCTCGSNQVCACQNSCQSC 482

RESULT 2
ID O62299 PRELIMINARY; PRT; 700 AA.
AC O62299;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein K03D10.1.
GN Name=K03D10.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
    investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA White S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA White S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81561; CAB04551.2; -.
DR EMBL; Z92828; CAB04551.2; JOINED.
DR EMBL; Z81561; CAB48500.1; JOINED.
DR EMBL; Z92828; CAB48500.1; -.
DR PIR; T23271; T23271.
DR WormPep; K03D10.1; CE18005.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 3.
DR PROSITE; PS00317; 4.DISULFIDE_CORE; 1.
DR PROSITE; PS0853; FN3; 2.
KW Hypothetical protein.
SQ SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;

Query Match 35.1%; Score 69.5; DB 2; Length 700;
Best Local Similarity 44.4%; Pred. No. 3.7;
Matches 12; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

QY 8 ECESICGADGAC---WTWCADGCSRSC 31
    |||::|||::|||::|||::|||
Db 117 ECSALCQMDGECFETQKCCSGCSRQC 143

RESULT 3
ID Q8WS94 PRELIMINARY; PRT; 700 AA.
AC Q8WS94;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

QY 8 ECESICGADGAC---WTWCADGCSRSC 31
    |||::|||::|||::|||::|||
Db 117 ECSALCQMDGECFETQKCCSGCSRQC 143

RESULT 4
ID CAB04551 PRELIMINARY; PRT; 700 AA.
AC CAB04551;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE C. elegans KAL-1 protein (Corresponding sequence K03D10.1).
GN KAL-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
    investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA White S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81561; CAB04551.2; -.
DR EMBL; Z92828; CAB04551.2; JOINED.
SQ SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;

Query Match 35.1%; Score 69.5; DB 2; Length 700;
Best Local Similarity 44.4%; Pred. No. 3.7;
Matches 12; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

QY 8 ECESICGADGAC---WTWCADGCSRSC 31
    |||::|||::|||::|||::|||
Db 117 ECSALCQMDGECFETQKCCSGCSRQC 143

RESULT 5
ID CAE48500 PRELIMINARY; PRT; 700 AA.
AC CAE48500;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ID CABA8500 PRELIMINARY; PRT; 700 AA.
AC CABA8500;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE C. elegans KAL-1 protein (Corresponding sequence K03D10.1).
GN KAL-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA White S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; 292828; CABA8500.1; -.
DR EMBL; 281561; CABA8500.1; JOINED.
SQ SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;

Query Match 35.1%; Score 69.5; DB 2; Length 700;
Best Local Similarity 44.4%; Pred. No. 3.7;
Matches 12; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

QY 8 ECESICGADGAC---WTWCADGCGSRSC 31
|||::|||::|||::|||::|||::|||::|||
Db 117 ECSALCQWDGCGPETOQKCCSSGCSRQC 143

RESULT 6
EZ3 MAIZE
ID EZ3 MAIZE STANDARD; PRT; 895 AA.
AC Q8S4P4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Polycarb protein EZ3 (Enhancer of zeste protein 3).
GN Name=EZ3; Synonyms=MEZ3;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Seed;
RX MEDLINE=21948211; PubMed=11950982; DOI=10.1104/pp.010742;
RA Springer N.M., Danilevskaya O.N., Hermon P., Helentjaris T.G.,
RA Phillips R.L., Kaeppler H.F., Kaeppler S.M.;
RT "Sequence relationships, conserved domains, and expression patterns
RT for maize homologs of the Polycarb group genes E(z), esc, and E(Pc).";
RL Plant Physiol. 128:1332-1345(2002).
CC -1- FUNCTION: Polycarb group (PcG) protein. PcG proteins act by
CC forming multiprotein complexes, which are required to maintain the
CC transcriptionally repressive state of homeotic genes throughout
CC development. PcG proteins are not required to initiate repression,
CC but to maintain it during later stages of development. They
CC probably act via the methylation of histones, rendering chromatin
CC heritably changed in its expressibility. Its sequence suggests
CC that it may participate in a potential methyltransferase activity
CC of PcG complexes (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: Belongs to the EZ family.
CC -1- SIMILARITY: Contains 1 SANT domain.

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CC -1- SIMILARITY: Contains 1 SET domain.
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CC -----
DR EMBL; AF443598; AAM13422.1; -.
DR MaizeDB; 754846; -.
DR InterPro; IPR001005; MYB_DNA_binding.
DR InterPro; IPR001214; SET.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00717; SANT; 1.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS50090; MYB 3; FALSE_NEG.
DR PROSITE; PS50280; SET; 1.
KW Multigene family; Nuclear protein; Repressor;
KW Transcription regulation.
FT DOMAIN 528 578 SANT.
FT DOMAIN 746 866 SET.
FT DOMAIN 650 719 Cys-rich.
FT DOMAIN 75 78 Poly-Ala.
SQ SEQUENCE 895 AA; 100392 MW; 2659DCF992A08919 CRC64;

Query Match 34.1%; Score 67.5; DB 1; Length 895;
Best Local Similarity 42.9%; Pred. No. 8.1;
Matches 15; Conservative 4; Mismatches 9; Indels 7; Gaps 3;

QY 2 YNLCTRECSICGADGAC---WTWCAD--GCSRSC 31
|||::|||::|||::|||::|||::|||::|||
Db 647 YNPCV--QQMGCKDCPCVENGTCCEKYCGCSKSC 679

RESULT 7
Q84UI6
ID Q84UI6 PRELIMINARY; PRT; 895 AA.
AC Q84UI6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Enhancer of zeste protein.
GN Name=ezi;
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22890056; PubMed=14527713;
RA Thakur J.K., Malik M., Bhatt V., Reddy M.K., Sopory S.K., Tyagi A.K.,
RA Khurana J.P.;
RT "A POLYCOMB group gene of rice (Oryza sativa L. subspecies indica),
RT OsEz1, codes for a nuclear-localized protein expressed preferentially
RT in young seedlings and during reproductive development.";
RL Gene 314:1-13(2003).
DR EMBL; AJ421722; CAD18871.3; -.
DR HSSP; P10968; 7MGA.
DR Gramene; Q84UI6; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001005; MYB_DNA_binding.
DR InterPro; IPR001214; SET.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00717; SANT; 1.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; UNKNOWN_1.
DR PROSITE; PS50280; SET; 1.
SQ SEQUENCE 895 AA; 99775 MW; BB618FCD0E414FA2 CRC64;

```

Query Match 34.1%; Score 67.5; DB 2; Length 895;
 Best Local Similarity 45.7%; Pred. No. 8.1;
 Matches 16; Conservative 3; Mismatches 9; Indels 7; Gaps 3;

OY 2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
 ||||| : : : : : ||||| : : : : :
 DB 647 YNPC--GCQMGCKDCACVNGTCCEKYCGSKSC 679

RESULT 8

Q8LLD6 PRELIMINARY; PRT; 895 AA.
 AC Q8LLD6;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE SET domain-containing protein.
 GN Name=SET1;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22751709; PubMed=12815033;
 RA Liang Y.-K., Wang Y., Zhang Y., Li S.-G., Lu X.-C., Li H., Zou C.,
 RA Xu Z.-H., Bai S.-N.;
 RT "OsSET1, a novel SET-domain-containing gene from rice.";
 RL J. Exp. Bot. 54:1995-1996(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liang Y., Bai S., Xu Z.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF407010; AA01115.1; -;
 DR HSSP; P10968; 7WGA.
 DR GRAMEN; Q8LLD6; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001005; MYD_DNA_binding.
 DR InterPro; IPR001214; SET.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF00856; SET; 1.
 DR SMART; SM00717; SANT; 1.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
 DR PROSITE; PS0280; SET; 1.
 SQ SEQUENCE 895 AA; 9980 MW; 47AA0F5DBFB7C84F CRC64;

Query Match 34.1%; Score 67.5; DB 2; Length 895;
 Best Local Similarity 45.7%; Pred. No. 8.1;
 Matches 16; Conservative 3; Mismatches 9; Indels 7; Gaps 3;

OY 2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
 ||||| : : : : : ||||| : : : : :
 DB 647 YNPC--GCQMGCKDCACVNGTCCEKYCGSKSC 679

RESULT 9

SIX2 LEIQU STANDARD; PRT; 82 AA.
 AC P19855; Q8MVS6; Q8MVS7; Q8MVS8;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Depressant insect toxin 2 precursor (Insect toxin LqgIT2).
 OS Leirus quinquestriatus quinquestriatus (Egyptian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthida; Buthoidea; Buthidae; Leirus.
 OX NCBI_TaxID=6885;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=22357239; PubMed=12467668;
 RA Zaki T.I., Maruniak J.E.;
 RT "Three polymorphic genes encoding a depressant toxin from the Egyptian
 scorpion Leirus quinquestriatus quinquestriatus.";
 RL Toxicon 41:109-113(2003).
 RN [2]
 RP SEQUENCE OF 22-82.
 RC TISSUE=Venom;
 RX MEDLINE=90184494; PubMed=2311768;
 RA Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E.M.,
 RA Rochat H., Granier C.;
 RT "Primary structure of scorpion anti-insect toxins isolated from the
 venom of Leirus quinquestriatus quinquestriatus.";
 RL FEBS Lett. 261:423-426(1990).
 RN [3]
 RP SEQUENCE OF 22-82.
 RC TISSUE=Venom;
 RX MEDLINE=91230120; PubMed=2029523;
 RA Zlotkin E., Eitan M., Bindokas V.P., Adams M.E., Moyer M.,
 RA Burkhardt W., Fowler E.;
 RT "Functional duality and structural uniqueness of depressant insect-
 selective neurotoxins.";
 RL Biochemistry 30:4814-4821(1991).
 RN [4]
 RP SEQUENCE OF 22-82.
 RC TISSUE=Venom;
 RX MEDLINE=93160530; PubMed=8431601;
 RA Zlotkin E., Gurevitz M., Fowler E., Adams M.E.;
 RT "Depressant insect selective neurotoxins from scorpion venom:
 chemistry, action, and gene cloning.";
 RL Arch. Insect Biochem. Physiol. 22:55-73(1993).
 RN [5]
 RP FUNCTION.
 RA Zlotkin E., Fowler E., Eitan M., Moyer M., Adams M.E.;
 RT "On the chemistry and action of the depressant insect toxins.";
 RL Toxicon 28:170-170(1990).
 CC -!- FUNCTION: Depressant insect toxins cause a transient contraction
 paralysis followed by a slow flaccid paralysis. They bind voltage-
 independently to sodium channels and block action potentials, the
 primarily by depolarizing the axonal membrane and suppressing the
 sodium current. This toxin induces a slow, depressant, flaccid
 paralysis on fly larvae. It is active only on insects.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-
 toxin subfamily.
 CC
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 CC
 DR EMBL; AF474983; AAM74027.1; -;
 DR EMBL; AF474984; AAM74028.1; -;
 DR EMBL; AF474985; AAM74029.1; -;
 DR PIR; B34123; B34123.
 DR HSSP; P01494; 2SN3.
 DR InterPro; IPR002061; Scorpion_toxinL.
 DR Pfam; PF00537; Toxin_3; 1.
 DR PRINTS; PR00285; SCORPNTOXIN.
 DR ProDom; PD000908; Scorpion_toxinL; 1.
 KW Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
 KW Polymorphism; Signal; Sodium channel inhibitor; Toxin.
 FT SIGNAL 1 21
 FT CHAIN 22 82 Depressant insect toxin 2.
 FT DISULFID 31 81 By similarity.
 FT DISULFID 35 56 By similarity.
 FT DISULFID 42 63 By similarity.
 FT DISULFID 46 65 By similarity.
 FT VARIANT 33 33 L -> V.

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FT VARIANT      43      43      N -> D.
FT VARIANT      48      48      S -> A.
FT VARIANT      71      71      D -> E.
SQ SEQUENCE    82 AA;  9099 MW;  F13D53B18CDCEBF0 CRC64;

Query Match
Best Local Similarity 33.8%; Score 67; DB 1; Length 82;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTW 22
   ||||| | : |||||
Db 42 CNKECKSYGGSYGICWTW 59

RESULT 10
HMCT_BOMMO
ID_HMCT_BOMMO STANDARD; PRT; 3133 AA.
AC P98092;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Hemocytin precursor (Humoral lectin).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI TaxID=7091;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Puyou X Tokai; TISSUE=Hemocyte;
RX MEDLINE=95178544; PubMed=7873598;
RA Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro M., Mori H., Sumida M.,
RA Matsubara F., Taniaki K., Kadono-Okuda K., Kato Y., Mori H.;
RT "Cloning and expression of the gene of hemocytin, an insect humoral
RT lectin which is homologous with the mammalian von Willebrand factor.";
RL Biochim. Biophys. Acta 1260:245-258(1995).
RN [2]
RP SEQUENCE OF 2221-3133 FROM N.A.
RA Kotani E., Iwamoto S.I., Tashiro M., Mori H., Sumida M., Matsubara F.,
RA Yamakawa M.;
RA Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Adhesive protein and relates to hemostasis or
CC encapsulation of foreign substances for self-defense.
CC -!- DEVELOPMENTAL STAGE: Expressed in hemocytes during larval-pupal
CC metamorphosis.
CC -!- INDUCTION: Hemagglutination activity is increased by bacterial or
CC viral infection and inhibited by D-mannose, N-acetyl-D-
CC galactosamine and D-maltose.
CC -!- PTM: May be converted into the 260 kDa mature hemocytin by
CC proteolysis.
CC -!- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 2 WFEC domains.
-----
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-----
CC EMBL; D29738; BAA06160.1; -.
CC EMBL; D14035; BAA03124.1; -.
CC PIR; S52093; S52093.
CC HSSP; P00451; 1IQD.
CC InterPro; IPR002919; Cysarich.TIL.
CC InterPro; IPR006207; Cys knot_C.
CC InterPro; IPR000421; FAS5_C.
CC InterPro; IPR008979; Gal_Bind_like.
CC InterPro; IPR009041; PMP_SGCI.
CC InterPro; IPR001007; VWF_C.
CC InterPro; IPR001846; VWF_D.

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DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF01826; TIL; 6.
DR Pfam; PF00094; VWD; 3.
DR DR PROSITE; PS01185; CTCK_1; 1.
DR DR PROSITE; PS01225; CTCK_2; 1.
DR DR PROSITE; PS01285; FAS5C_1; 2.
DR DR PROSITE; PS01286; FAS5C_2; 2.
DR DR PROSITE; PS00022; FAS5C_3; 2.
DR DR PROSITE; PS01208; WFEC_1; FALSE NEG.
KW Cell adhesion; Glycoprotein; Lectin; Repeat; Signal.
FT SIGNAL 1 ?
FT CHAIN ? 3133 Hemocytin.
FT DOMAIN 29 131 D'.
FT DOMAIN 153 240 D'.
FT DOMAIN 248 613 D1.
FT DOMAIN 940 1095 F5/8 type C 1.
FT DOMAIN 1116 1254 F5/8 type C 2.
FT DOMAIN 1283 1356 D''.
FT DOMAIN 1620 1951 D2.
FT DOMAIN 1952 2315 D3.
FT DOMAIN 2230 2321 C-TYPE LECTIN (ATYPICAL).
FT DOMAIN 2335 2361 B1.
FT DOMAIN 2435 2469 B2.
FT DOMAIN 2553 2622 WFEC 1.
FT DOMAIN 2842 2907 WFEC 2.
FT DOMAIN 2971 3076 CTCK.
FT DOMAIN 895 914 Poly-Thr.
FT DOMAIN 1267 1270 Poly-Glu.
FT DOMAIN 1425 1428 Poly-Thr.
FT DOMAIN 1447 1450 Poly-Thr.
FT DOMAIN 1474 1479 Poly-Ser.
FT DOMAIN 2148 2153 Poly-Pro.
FT DOMAIN 2156 2159 Poly-Pro.
FT DOMAIN 2341 2344 Poly-Pro.
FT DISULFID 940 1095 By similarity.
FT DISULFID 1116 1254 By similarity.
FT DISULFID 2981 3040 By similarity.
FT DISULFID 2991 3054 By similarity.
FT DISULFID 3004 3070 By similarity.
FT DISULFID 3020 3072 By similarity.
FT DISULFID ? 3075 By similarity.
FT CARBOHYD 151 151 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 237 237 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 564 564 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1170 1170 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1387 1387 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1622 1622 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1727 1727 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1847 1847 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1975 1975 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1985 1985 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2093 2093 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2113 2113 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2161 2161 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2276 2276 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2451 2451 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2647 2647 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2654 2654 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2663 2663 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2794 2794 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2810 2810 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2865 2865 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2929 2929 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 2964 2964 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 3028 3028 N-linked (GlcNAc... ) (Potential).
FT VARIANT 1288 1288 R -> G.
FT VARIANT 1305 1305 T -> S.
SQ SEQUENCE 3133 AA; 343350 MW; E5210D5D14A7B2B2 CRC64;

Query Match 33.1%; Score 65.5; DB 1; Length 3133;
Best Local Similarity 46.7%; Pred. No. 43;
Matches 14; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

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QY 2 YNLIRECESICGADGACWTWCADGCSRSC 31
 Db 31 YN--VKCELSCTGGQQYTVCAADSLRKC 57

RESULT 11

LCR1 ARATH
 ID LCR1 ARATH STANDARD; PRT; 89 AA.
 AC P82716;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Low-molecular-weight cysteine-rich protein LCR1 precursor.
 GN Name=LCR1;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:31-63 (2000).
 RN [2]

RP IDENTIFICATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=21330246; PubMed=11437247; DOI=10.1023/A:1010664704926;
 RA Vancosthuyse V., Mieghe C., Dumas C., Cock J.M.;
 RT "Two large Arabidopsis thaliana gene families are homologous to the
 RT Brassica gene superfamily that encodes pollen coat proteins and the
 RT male component of the self-incompatibility response.";
 RL Plant Mol. Biol. 46:17-34 (2001).
 CC -!- TISSUE SPECIFICITY: Expressed in flower buds, but not in stems,
 CC roots or rosette leaves.

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DR EMBL; AB020745; -; NOT ANNOTATED_CDS.
 DR InterPro; IPR010851; SLR1-BP.
 DR Pfam; PF07333; SLR1-BP; 1.
 KW Multigene family, Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 89 Low-molecular-weight cysteine-rich
 FT protein LCR1.
 FT SEQUENCE 89 AA; 10016 MW; 383A5E84C1380114 CRC64;

Query Match 32.8%; Score 65; DB 1; Length 89;
 Best Local Similarity 41.4%; PRT; No. 2.1;
 Matches 12; Conservative 6; Mismatches 5; Indels 6; Gaps 2;

QY 4 LCI-RECESIC-----GADGACWTWCADG 26
 Db 45 LCVLKDCEVCKTKSGLEGICWKNKNG 73

RESULT 12

Q8BRC8
 ID Q8BRC8 PRELIMINARY; PRT; 101 AA.

AC Q8BRC8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
 DE enriched library, clone:B130034E13 product:hypothetical protein, full
 DE insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tgami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK045114; BAC32228.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 101 AA; 10965 MW; 4B5CFB2479BB1AF CRC64;
 Query Match 32.8%; Score 65; DB 2; Length 101;
 Best Local Similarity 32.3%; PRT; No. 2.3;

```

Matches 10; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 CYNLCIRCESICGADGACWTWCADGCSRS 31
Db 10 CVCVCVCVCVCVCVCARACDRYCSHACARYC 40

RESULT 13
Q7UNP4
ID Q7UNP4 PRELIMINARY; PRT; 838 AA.
AC Q7UNP4;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB7455;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Firellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294146; CAD75374.1; -.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR011521; YTV.
DR Pfam; PF07639; YTV; 5.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 838 AA; 92235 MW; 84AD168706763544 CRC64;

Query Match 32.8%; Score 65; DB 2; Length 838;
Best Local Similarity 46.2%; Pred. No. 15;
Matches 12; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTWCADGCSRS 30
Db 438 CGGCGASSCGSCSACTACSGDGGSGS 463

RESULT 14
Q6NP04
ID Q6NP04 PRELIMINARY; PRT; 591 AA.
AC Q6NP04;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE LD02520p (Fragment).
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BT011127; AAR82794.1; -.

Query Match 32.6%; Score 64.5; DB 2; Length 591;
Best Local Similarity 41.4%; Pred. No. 13;
Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 2;

QY 5 CIREC--ESICGADGACWTWCADGCSRS 31
Db 162 CARECTYDADCRGNKC---CSDGCGQLC 187

Search completed: November 16, 2004, 14:29:44

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DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00900; PLAC; 1.
FT NON_TER 1
SQ SEQUENCE 591 AA; 64870 MW; D08400487404CFE8 CRC64;

Query Match 32.6%; Score 64.5; DB 2; Length 591;
Best Local Similarity 41.4%; Pred. No. 13;
Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 2;

QY 5 CIREC--ESICGADGACWTWCADGCSRS 31
Db 162 CARECTYDADCRGNKC---CSDGCGQLC 187

RESULT 15
AAR82794
ID AAR82794 PRELIMINARY; PRT; 591 AA.
AC AAR82794;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE LD02520p (Fragment).
GN PPN.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT011127; AAR82794.1; -.
FT NON_TER 1
SQ SEQUENCE 591 AA; 64870 MW; D08400487404CFE8 CRC64;

Query Match 32.6%; Score 64.5; DB 2; Length 591;
Best Local Similarity 41.4%; Pred. No. 13;
Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 2;

QY 5 CIREC--ESICGADGACWTWCADGCSRS 31
Db 162 CARECTYDADCRGNKC---CSDGCGQLC 187

Search completed: November 16, 2004, 14:29:44

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Job time : 186.83 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:09:48 ; Search time 51.283 Seconds
(without alignments)
62.956 Million cell updates/sec

Title: US-10-784-537-2

Perfect score: 57

Sequence: 1 CPRECECIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_238Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	57	100.0	9	5	ABG60448	Abg60448 Selective
2	57	100.0	9	6	ABR56860	AbR56860 Aminopept
3	50	87.7	13	5	ABG60452	Abg60452 Selective
4	50	87.7	13	6	ABR56864	AbR56864 Aminopept
5	47	82.5	31	5	ABG60450	Abg60450 Selective
6	47	82.5	31	6	ABR56862	AbR56862 Aminopept
7	44	77.2	58	4	RAAG74702	RAAG74702 Human col
8	43	75.4	460	4	RAAM38740	RAAM38740 Human pol
9	43	75.4	501	5	ABG70171	ABG70171 Human pre
10	43	75.4	512	4	RAAM40526	RAAM40526 Human pol
11	40	70.2	13	2	RAAW13427	RAAW13427 Breast tu
12	40	70.2	13	2	RAAW60290	RAAW60290 Breast ca
13	40	70.2	13	2	RAAW93627	RAAW93627 Breast tu
14	40	70.2	13	3	RAAB17959	RAAB17959 Integrin-
15	40	70.2	13	3	RAAB17923	RAAB17923 VEGF anta
16	40	70.2	13	3	RAAB21702	RAAB21702 Human bre
17	40	70.2	13	4	RAA06280	RAA06280 Human bre
18	40	70.2	13	5	RAAU81104	RAAU81104 Integrin-
19	40	70.2	13	7	ABb72956	ABb72956 Integrin
20	40	70.2	13	7	ADJ73110	ADJ73110 Integrin
21	40	70.2	13	8	ADJ52745	ADJ52745 CHI delet
22	40	70.2	13	8	ADJ51706	ADJ51706 CHI delet
23	40	70.2	43	4	RAE03911	RAE03911 Human gen
24	40	70.2	43	5	ABb57419	ABb57419 Human sec
25	40	70.2	43	6	ADA98407	ADA98407 Human sec

26	40	70.2	43	6	ADA98405	Ada98405 Human sec
27	40	70.2	43	6	ADA98404	Ada98404 Human sec
28	40	70.2	43	6	ADA98396	Ada98396 Human sec
29	40	70.2	43	6	ADA44203	Ada44203 Human sec
30	40	70.2	43	6	ADA44191	Ada44191 Human sec
31	40	70.2	43	6	ADA44205	Ada44205 Human sec
32	40	70.2	43	6	ADA44202	Ada44202 Human sec
33	40	70.2	43	7	ADC20563	ADC20563 Human sec
34	40	70.2	43	7	ADC20579	ADC20579 Human sec
35	40	70.2	43	7	ADC20581	ADC20581 Human sec
36	40	70.2	43	7	ADC20578	ADC20578 Human sec
37	40	70.2	43	7	ADF10801	ADF10801 Human sec
38	40	70.2	43	7	ADF10806	ADF10806 Human sec
39	40	70.2	43	7	ADF10807	ADF10807 Human sec
40	40	70.2	43	7	ADF10809	ADF10809 Human sec
41	40	70.2	44	4	AAU01745	AAU01745 Human sec
42	40	70.2	44	4	AAU01069	AAU01069 Human sec
43	40	70.2	44	4	AAU01949	AAU01949 Human sec
44	40	70.2	44	4	AAB60747	AAB60747 Human sec
45	40	70.2	63	7	ADE11750	ADE11750 Human sec

ALIGNMENTS

RESULT 1
ABG60448
ID ABG60448 standard; peptide; 9 AA.
XX
AC ABG60448;
XX
DT 30-JUL-2002 (first entry)
XX
DE Selective targeting peptide #123.
XX
KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
KW gene therapy.
XX
OS Synthetic.
XX
PN WO200220769-A1.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-US027692.
XX
PR 08-SEP-2000; 2000US-0231266P.
PR 17-JAN-2001; 2001US-00765101.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Arap W, Pasqualini R;
XX
DR WPI; 2002-415731/44.
XX
PT Targeting peptides identified by phage display, useful for targeting
PT delivery to an organ or tissue, particularly for treating a disease, e.g.
PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
PT disease.
XX
PS Claim 22; Page 102; 317pp; English.
XX
CC The invention relates to an isolated peptide of 100 amino acids or less
CC in size useful for targeting delivery to an organ or tissue, particularly
CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
CC infection, cardiovascular disease or degenerative disease. The peptide is
CC also useful for inducing apoptosis, particularly to a subject with
CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

CC inflammation or macular degeneration. Furthermore, the peptide is useful
CC for diagnosing the diseases cited above. Targeting peptides of the
CC invention can also be used to deliver an agent to a foetus, by attaching
CC a peptide to the agent and administering the peptide to a pregnant
CC subject. Sequences ABG60326-ABG60574 represent selective targeting
CC peptides of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 57; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECESIC 9
| | | | |
Db 1 CPRECESIC 9

RESULT 2

ABR56860
ID ABR56860 standard; peptide; 9 AA.

AC ABR56860;

DT 30-JUL-2003 (first entry)

DE Aminopectidase A (APA) binding peptide SEQ ID NO:56.

XX Targeting peptide; obesity; lipodystrophy; anorectic; antilipaemic;
KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
KW beta-3 integrin; beta-5 integrin; spleen; amineopeptidase A.

XX Synthetic.

OS WO2003022991-A2.

PN 20-MAR-2003.

PP 30-AUG-2002; 2002WO-US027836.

PR 07-SEP-2001; 2001WO-US027692.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Pasqualini R, Arap W, Kolonin MG;

DR WPI; 2003-371749/35.

XX Treating obesity or a lipodystrophy comprises obtaining a targeting
PT peptide selective for adipose tissue, attaching the peptide to a
PT therapeutic agent to form a complex, and administering the complex to a
PT subject.

PS Example 8; Page 98; 247pp; English.

XX The present invention describes a method for treating obesity or a
CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
CC agent to form a complex; (c) administering the complex to a subject; and
CC (d) inducing weight loss in the subject or treating lipodystrophy. The
CC adipose targeting peptides have anorectic and antilipaemic activities,
CC and can be used in peptide and gene therapy. The method is used for
CC treating obesity or a lipodystrophy that is related to infection with
CC human immunodeficiency virus (HIV). The peptides used in the method can
CC also be used for targeting delivery to an organ or tissue, such as
CC placental delivery. A receptor that binds to a placenta targeting peptide
CC is used to screen compounds for teratogenic activity. ABR56806 to
CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
CC exemplification of the present invention

XX Sequence 9 AA;

Query Match 100.0%; Score 57; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECESIC 9
| | | | |
Db 1 CPRECESIC 9

RESULT 3

ABG60452
ID ABG60452 standard; peptide; 13 AA.

AC ABG60452;

DT 30-JUL-2002 (first entry)

DE Selective targeting peptide #127.

XX Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
KW gene therapy.

XX Synthetic.

PN WO200220769-A1.

XX 14-MAR-2002.

PP 07-SEP-2001; 2001WO-US027692.

PR 08-SEP-2000; 2000US-0231266P.

PR 17-JAN-2001; 2001US-00765101.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;

DR WPI; 2002-415731/44.

XX Targeting peptides identified by phage display, useful for targeting
PT delivery to an organ or tissue, particularly for treating a disease, e.g.
PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
PT disease.

PS Claim 22; Page 109; 317pp; English.

XX The invention relates to an isolated peptide of 100 amino acids or less
CC in size useful for targeting delivery to an organ or tissue, particularly
CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
CC infection, cardiovascular disease or degenerative disease. The peptide is
CC also useful for inducing apoptosis, particularly to a subject with
CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
CC inflammation or macular degeneration. Furthermore, the peptide is useful
CC for diagnosing the diseases cited above. Targeting peptides of the
CC invention can also be used to deliver an agent to a foetus, by attaching
CC a peptide to the agent and administering the peptide to a pregnant
CC subject. Sequences ABG60326-ABG60574 represent selective targeting
CC peptides of the invention

XX Sequence 13 AA;

Query Match 87.7%; Score 50; DB 5; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECESIC 9
| | | | |
Db 5 CPRECESIC 13

RESULT 4
 ABR56864
 ID ABR56864 standard; peptide; 13 AA.
 XX
 AC ABR56864;
 XX
 DT 30-JUL-2003 (first entry)
 XX
 DE Aminopectidase A (APA) binding peptide SEQ ID NO:60.
 XX
 KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipemic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; adipose; aminopeptidase A.
 XX
 OS Synthetic.
 XX
 PN WO2003022991-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027836.
 XX
 PR 07-SEP-2001; 2001WO-US027692.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Pasqualini R, Arap W, Kolonin MG;
 XX
 DR WPI; 2003-371749/35.
 XX
 PT Treating obesity or a lipodystrophy comprises obtaining a targeting
 PT peptide selective for adipose tissue, attaching the peptide to a
 PT therapeutic agent to form a complex, and administering the complex to a
 PT subject.
 XX
 PS Example 8; Page 104; 247pp; English.
 XX
 CC The present invention describes a method for treating obesity or a
 CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
 CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
 CC agent to form a complex; (c) administering the complex to a subject; and
 CC (d) inducing weight loss in the subject or treating lipodystrophy. The
 CC adipose targeting peptides have anorectic and antilipemic activities,
 CC and can be used in peptide and gene therapy. The method is used for
 CC treating obesity or a lipodystrophy that is related to infection with
 CC human immunodeficiency virus (HIV). The peptides used in the method can
 CC also be used for targeting delivery to an organ or tissue, such as
 CC placental delivery. A receptor that binds to a placenta targeting peptide
 CC is used to screen compounds for teratogenic activity. ABR56806 to
 CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 13 AA;
 Query Match 87.7%; Score 50; DB 6; Length 13;
 Best Local Similarity 88.9%; Pred. NO. 1.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CPRECESIC 9
 Db |||||
 5 CPRECESNC 13
 RESULT 5
 ABR56450
 ID ABR56450 standard; peptide; 31 AA.
 XX
 AC ABR56450;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Aminopectidase A (APA) binding peptide SEQ ID NO:58.
 XX
 KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipemic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; adipose; aminopeptidase A.

XX
 DE Selective targeting peptide #125.
 XX
 KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO200220769-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US027692.
 XX
 PR 08-SEP-2000; 2000US-0231266P.
 PR 17-JAN-2001; 2001US-00765101.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Arap W, Pasqualini R;
 XX
 DR WPI; 2002-415731/44.
 XX
 PT Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease, e.g.
 PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
 PT disease.
 XX
 PS Claim 22; Page 108; 317pp; English.
 XX
 CC The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABR560326-ABR560574 represent selective targeting
 CC peptides of the invention
 XX
 SQ Sequence 31 AA;
 Query Match 82.5%; Score 47; DB 5; Length 31;
 Best Local Similarity 88.9%; Pred. NO. 6.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CPRECESIC 9
 Db |||||
 5 CPRECESIC 13
 RESULT 6
 ABR56862
 ID ABR56862 standard; peptide; 31 AA.
 XX
 AC ABR56862;
 XX
 DT 30-JUL-2003 (first entry)
 XX
 DE Aminopectidase A (APA) binding peptide SEQ ID NO:58.
 XX
 KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipemic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; adipose; aminopeptidase A.

```

XX OS Synthetic.
XX PN WO2003022991-A2.
XX PD 20-MAR-2003.
XX PF 30-AUG-2002; 2002WO-US027836.
XX PR 07-SEP-2001; 2001WO-US027692.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Pasqualini R, Arap W, Kolonin MG;
XX DR WPI; 2003-371749/35.
XX PT Treating obesity or a lipodystrophy comprises obtaining a targeting
XX PT peptide selective for adipose tissue, attaching the peptide to a
XX PT therapeutic agent to form a complex, and administering the complex to a
XX PT subject.
XX PS Example 8; Page 104; 247pp; English.
XX CC The present invention describes a method for treating obesity or a
XX CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
XX CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
XX CC agent to form a complex; (c) administering the complex to a subject; and
XX CC (d) inducing weight loss in the subject or treating lipodystrophy. The
XX CC adipose targeting peptides have anorectic and antilipemic activities,
XX CC and can be used in peptide and gene therapy. The method is used for
XX CC treating obesity or a lipodystrophy that is related to infection with
XX CC human immunodeficiency virus (HIV). The peptides used in the method can
XX CC also be used for targeting delivery to an organ or tissue, such as
XX CC placental delivery. A receptor that binds to a placenta targeting peptide
XX CC is used to screen compounds for teratogenic activity. ABR56806 to
XX CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 31 AA;

    Query Match      82.5%; Score 47; DB 6; Length 31;
    Best Local Similarity 88.9%; Pred. No. 6.3;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
DB 5 CIRECESIC 13

    RESULT 7
    AAG74702
    ID AAG74702 standard; protein; 58 AA.
    AC AAG74702;
    XX
    DT 03-SEP-2001 (first entry)
    DE Human colon cancer antigen protein SEQ ID NO:5466.
    XX
    KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
    KW colorectal carcinoma.
    XX
    OS Homo sapiens.
    XX
    PN WO200122920-A2.
    XX
    PD 05-APR-2001.
    XX
    PF 28-SEP-2000; 2000WO-US026524.
    XX
    PR 29-SEP-1999; 99US-0157137P.
    PR 03-NOV-1999; 99US-0163280P.
    PR

(HUMA-) HUMAN GENOME SCI INC.
Ruben SM, Barash SC, Birse CE, Rosen CA;
WPI; 2001-235357/24.
N-PSDB; AAH34107.
Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
useful for preventing, diagnosing and/or treating colorectal cancers.
Claim 11; Page 7070-7071; 9803pp; English.
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
cancer-associated nucleic acid molecules (N) and proteins (P), where the
proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene therapy
and vaccine production. N and P may be used in the prevention, diagnosis
and treatment of diseases associated with inappropriate P expression. For
example, N and P may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of P by expressing inactive proteins or to
supplement the patients own production of P. Additionally, N may be used
to produce the colon cancer-associated PS, by inserting the nucleic acids
into a host cell and culturing the cell to express the proteins. N and P
can be used in the prevention, diagnosis and treatment of colorectal
carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
sequences used in the exemplification of the present invention. N.B.
Pages 666 to 682 and page 7053 of the sequence listing were missing at
time of publication, meaning no sequences are present for SEQ ID NO:1027
to 1052, 7921 and 7922
Sequence 58 AA;

    Query Match      77.2%; Score 44; DB 4; Length 58;
    Best Local Similarity 66.7%; Pred. No. 29;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
DB 29 CPRECSFLC 37

    RESULT 8
    AAM38740
    ID AAM38740 standard; protein; 460 AA.
    AC AAM38740;
    XX
    DT 22-OCT-2001 (first entry)
    DE Human polypeptide SEQ ID NO 1885.
    XX
    KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
    KW peripheral nervous system; neuropathy; central nervous system; CNS;
    KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
    KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
    KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
    KW leukaemia.
    XX
    OS Homo sapiens.
    XX
    PN WO200153312-A1.
    XX
    PD 26-JUL-2001.
    XX
    PF 26-DEC-2000; 2000WO-US034263.
    XX
    PR 23-DEC-1999; 99US-00471275.
    PR 21-JAN-2000; 2000US-00488725.
    PR 25-APR-2000; 2000US-00552317.
    PR 20-JUN-2000; 2000US-00598042.
    PR 19-JUL-2000; 2000US-00620312.
    PR

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PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00682191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AAI57896.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 3; SEQ ID NO 1885; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 460 AA;
XX
XX Query Match 75.4%; Score 43; DB 4; Length 460;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 CPRECECIC 9
Db |||:::
439 CPQCEPAVC 447
XX
RESULT 9
ABG70171
XX ABG70171 standard; protein; 501 AA.
XX
XX ABG70171;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human prey protein for Shigella ipaH9.8 #1.
XX
XX Prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella;
KW Shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system;
KW protein-protein interaction; SID; selected interacting domain; human.
XX
XX Homo sapiens.
XX
XX WO200257303-A2.
XX
XX 25-JUL-2002.
XX
XX 11-JAN-2002; 2002WO-EP000777.
XX
XX 12-JAN-2001; 2001US-0261130P.
XX
XX (HYBR-) HYBRIGENICS.
XX
XX Legrain P;
XX
XX WPI: 2002-599706/64.
DR N-PSDB; ABS51564.
XX
XX New complex of protein-protein interactions between a bait Shigella
PT flexneri polypeptide and a prey mammalian or human placenta polypeptide
PT for treating or preventing bacillary dysentery in a mammal or human.
XX
XX Claim 7; Page 116-117; 162pp; English.
XX
XX The invention relates to a complex of protein-protein interactions
CC between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC,
CC ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the
CC specification. The complexes are formed using the yeast two-hybrid
CC system. Also included are (1) a recombinant host cell expressing the
CC interactions between the Shigella flexneri polypeptide and a mammalian
CC polypeptide defined in the specification; (2) selecting a modulating
CC compound that inhibits or activates the protein-protein interactions; (3)
CC a modulating compound obtained from the method of (2); (4) a SID
CC (selected interacting domain) polypeptide or its fragment or variant
CC comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a
CC SID polynucleotide or its fragment or variant comprising encoding the
CC above polypeptides a vector comprising (5); (6) a recombinant host cell
CC containing the vector; and (10) a protein chip comprising Shigella
CC flexneri polypeptide and a mammalian polypeptide defined in the
CC specification. A pharmaceutical composition comprising the compound,
CC polypeptide or polynucleotide is useful for treating or preventing
CC shigellosis (bacillary dysentery) in a human or mammal. The present
CC sequence represents a human prey protein isolated by the yeast two-hybrid
CC assay, forming a complex of the invention with a shigella protein
XX
XX Sequence 501 AA;
XX
XX Query Match 75.4%; Score 43; DB 5; Length 501;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2 PRECECIC 9
Db |||||::|
33 PRECEPIC 40
XX
RESULT 10
AAM40526
XX ID AAM40526 standard; protein; 512 AA.
XX
XX AAM40526;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 5457.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.

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PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-P8DB; AAI59682.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 5457; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAW42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX SQ Sequence 512 AA;

Query Match 75.4%; Score 43; DB 4; Length 512;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
Db 491 CPQECPAVC 499
||:|:|:|

RESULT 11
AAW13427
ID AAW13427 standard; peptide; 13 AA.
XX
XX AAW13427;
XX
DT 15-JAN-1998 (first entry)
XX
XX Breast tumour homing peptide.
DE
DE Breast tumour homing peptide; cancer; in vivo panning; screening;
KW phage display; drug delivery.
KW
XX Synthetic.
OS
XX WO9710507-A1.
PN
XX 20-MAR-1997.
PD
XX 10-SEP-1996; 96WO-US014600.
PF
XX 11-SEP-1995; 95US-00526708.
PR
XX 11-SEP-1995; 95US-00526710.
XX
XX (LJOL-) LA JOLLA CANCER RES FOUND.
PA
XX Ruoslahti E, Pasqualini R;
PI
XX

DR WPI; 1997-202359/18.
XX
XX Obtaining compound that homes to selected organ or tissue - by in vivo
PT panning method, specifically to identify brain, kidney, angiogenic
PT vasculature or tumour tissue homing peptide(s).
XX
XX Claim 18; Page 68; 75pp; English.
XX
XX This synthetic peptide is a claimed example of a breast tumour-homing
CC peptide that was identified using a novel method for obtaining molecules
CC that home to a selected organ or tissue. This in vivo panning method
CC typically involves administering a phage display library to a subject,
CC and identifying expressed peptides which home to the desired organ or
CC tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue.
CC The isolated peptides (see AAW13412-52, AAW1181-86) can be used to
CC target e.g. drugs, toxins or labels to the selected organ/tissue
CC (claimed) or to identify and/or isolate target molecules (claimed). The
CC peptides can be directly identified in vivo, as compared to prior art in
CC vitro screening methods, which require further examination to see if they
CC maintain specificity in vivo
XX
XX SQ Sequence 13 AA;

Query Match 70.2%; Score 40; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
Db 5 CPRLCQSSC 13
|||:|:|

RESULT 12
AAW60290
ID AAW60290 standard; peptide; 13 AA.
XX
XX AAW60290;
AC
XX 24-AUG-1998 (first entry)
DT
XX
XX Breast carcinoma tumour homing peptide of the invention.
DE
XX Tumour homing peptide; in vivo panning; breast carcinoma;
KW alpha-V-containing integrin binding motif; tumour.
KW
XX Unidentified.
OS
XX WO9810795-A2.
PN
XX 19-MAR-1998.
PD
XX 10-SEP-1997; 97WO-US016086.
PF
XX 10-SEP-1996; 96US-00710067.
PR
XX (BURN-) BURNHAM INST.
XX
XX Ruoslahti E, Pasqualini R;
PI
XX WPI; 1998-207151/18.
PN
XX Tumour homing molecules and their conjugates - useful for, e.g. directing
PT linked moiety to tumour containing angiogenic vasculature.
PT
XX Disclosure; Page 6; 105pp; English.
PS
XX The present peptide represents a tumour homing peptide, and is produced
CC by in vivo panning. The peptide homes to a breast carcinoma. The in vivo
CC panning comprises administering a library of diverse peptides to a
CC subject having a tumour, collecting a sample of the tumour, identifying a
CC peptide that homes to the tumour, collecting a sample of normal tissue
CC corresponding to the tumour, and determining that the peptide that homes
CC to the tumour is not present in the normal tissue. The tumour homing

CC peptide can be linked to a moiety (e.g. doxorubicin), and used to direct
 CC the moiety to a tumour
 XX
 SQ Sequence 13 AA;
 Query Match 70.2%; Score 40; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CPRECECIC 9
 |||||:
 Db 5 CPRLCQSSC 13

RESULT 13
 AAW93627
 ID AAW93627 standard; protein; 13 AA.
 XX
 AC AAW93627;
 XX
 DT 28-JUN-1999 (first entry)
 XX
 DE Breast tumour homing peptide 1.
 XX
 KW Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
 KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
 KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
 KW prognosis; inflammation; regeneration; wounded tissue; targeting;
 KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
 KW occlusive thrombus.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9913329-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 08-SEP-1998; 98WO-US018895.
 XX
 PR 10-SEP-1997; 97US-00926914.
 PR 25-AUG-1998; 98US-00139802.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Ruoslahti E, Pasqualini R;
 XX
 DR WPI; 1999-215158/18.
 XX
 PT Identifying molecules that home to angiogenic vasculature used as targets
 PT for anticancer agents.
 XX
 PS Example II; Page 67; 180pp; English.
 XX
 CC This invention describes novel peptides which home to angiogenic
 CC vasculature, specifically of a tumour and which have anti-tumour, anti-
 CC inflammatory, anti-angiogenic and anti-arthritis activity. Such molecules
 CC are identified by treating a purified NGR receptor with a test compound
 CC and identifying compounds that bind specifically to the NGR receptor. The
 CC peptides of the invention are inhibitors of angiogenesis and can be used
 CC to produce conjugates for delivering agents to angiogenic vasculature,
 CC particularly anticancer drugs or an imaging agent, for diagnosis or
 CC prognosis. These conjugates may be directed to non-tumour angiogenic
 CC vasculature, e.g. that present in inflammatory, regenerating or wounded
 CC tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
 CC or rheumatoid arthritis. The peptides provide specific targeting to
 CC tumours, especially their supporting vasculature, since the NGR receptor
 CC is exposed to the circulation only in angiogenic vasculature. Precise
 CC targeting should reduce the systemic toxicity of anticancer drugs in the
 CC conjugates. Complete killing of all target cells may not be essential
 CC since partial denudation of endothelium may result in an occlusive
 CC thrombus, and endothelial cells are unlikely to become resistant to
 CC anticancer agents nor to lose the targeting receptor. AAW93622-W93809 and

CC AAW93843-44 are examples of tumour homing peptides used in the invention
 XX
 SQ Sequence 13 AA;
 Query Match 70.2%; Score 40; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CPRECECIC 9
 |||||:
 Db 5 CPRLCQSSC 13

RESULT 14
 AAB17959
 ID AAB17959 standard; peptide; 13 AA.
 XX
 AC AAB17959;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Integrin-binding peptide sequence SEQ ID NO:1071.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US025044.
 XX
 PR 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Claim 39; Page 589; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAB17959 to AAB17955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 13 AA;

Query Match 70.2%; Score 40; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPRECECISIC 9
||| |:
Db 5 CPRLCQSSC 13

RESULT 15

AAB17923
ID AAB17923 standard; peptide; 13 AA.

XX AC

XX AC

DT 31-OCT-2000 (first entry)

XX VEGF antagonist peptide sequence SEQ ID NO:1027.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.

XX OS

XX Synthetic.

XX PN W0200024782-A2.

XX PD 04-MAY-2000.

XX PF 25-OCT-1999; 99WO-US025044.

XX PR 23-OCT-1998; 98US-0105371P.

XX PR 22-OCT-1999; 99US-00428082.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham J, Boone TC;

XX DR WPI; 2000-350702/30.

XX PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.

XX PS Claim 39; Page 557; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention

XX SQ Sequence 13 AA;

Query Match 70.2%; Score 40; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 31;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CPRECECISIC 9
||| |:
Db 5 CPRLCQSSC 13

Search completed: November 16, 2004, 14:24:26
Job time : 59.283 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:16:01 ; Search time 12.7358 Seconds
(without alignments)
46.865 Million cell updates/sec

Title: US-10-784-537-2

Perfect score: 57

Sequence: 1 CPRECECIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	70.2	13	4	US-09-659-786-2
3	40	70.2	13	4	US-08-926-914-2
4	40	70.2	13	4	US-09-428-082B-1071
5	40	70.2	58	4	US-09-270-767-57784
6	40	70.2	118	4	US-09-270-767-42488
7	40	70.2	596	4	US-09-252-991A-26031
8	40	70.2	816	2	US-08-820-170A-37
9	40	70.2	816	3	US-09-055-699-37
10	40	70.2	816	3	US-09-273-565-37
11	40	70.2	816	3	US-09-565-538-37
12	40	70.2	816	3	US-09-661-468-37
13	40	70.2	816	4	US-09-976-165-37
14	39	68.4	699	4	US-09-538-092-995
15	39	68.4	723	4	US-09-543-681A-5457
16	38	66.7	13	3	US-09-139-802-2
17	38	66.7	13	4	US-09-659-786-2
18	38	66.7	13	4	US-08-926-914-2
19	37	64.9	107	4	US-09-107-532A-3965
20	37	64.9	194	3	US-08-480-640A-196
21	37	64.9	194	3	US-08-686-968C-196
22	37	64.9	194	3	US-08-488-237A-196
23	37	64.9	194	3	US-08-375-992A-196
24	37	64.9	194	4	US-08-472-679H-196
25	37	64.9	417	3	US-08-815-469-4
26	37	64.9	417	3	US-09-153-927-2
27	37	64.9	417	4	US-09-565-918-5

28	37	64.9	417	4	US-08-928-069-10	Sequence 10, Appli
29	37	64.9	417	4	US-08-828-683A-6	Sequence 6, Appli
30	37	64.9	417	4	US-09-557-908-4	Sequence 4, Appli
31	37	64.9	417	4	US-09-874-138-5	Sequence 5, Appli
32	37	64.9	417	4	US-09-333-966-4	Sequence 2, Appli
33	37	64.9	428	3	US-08-815-469-2	Sequence 2, Appli
34	37	64.9	428	4	US-09-557-908-2	Sequence 2, Appli
35	37	64.9	428	4	US-09-333-966-2	Sequence 2, Appli
36	37	64.9	470	3	US-08-813-150-2	Sequence 2, Appli
37	37	64.9	470	4	US-09-546-553-2	Sequence 2, Appli
38	37	64.9	478	4	US-09-134-000C-5543	Sequence 5543, Ap
39	37	64.9	833	3	US-09-013-895A-5	Sequence 5, Appli
40	37	64.9	833	4	US-09-448-868-5	Sequence 5, Appli
41	37	64.9	859	4	US-09-538-092-206	Sequence 206, App
42	37	64.9	1015	1	US-08-537-210A-1	Sequence 1, Appli
43	37	64.9	1015	3	US-09-113-825-1	Sequence 1, Appli
44	37	64.9	2471	1	US-08-185-432-16	Sequence 16, Appli
45	37	64.9	2471	1	US-08-083-590A-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1

US-09-139-802-2

; Sequence 2, Application US/09139802

; Patent No. 6180084

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing

; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: P-LJ 3203

; CURRENT APPLICATION NUMBER: US/09/139,802

; CURRENT FILING DATE: 1998-08-25

; EARLIER APPLICATION NUMBER: 08/926,914

; EARLIER FILING DATE: 1997-09-10

; EARLIER APPLICATION NUMBER: 08/710,067

; EARLIER FILING DATE: 1996-09-10

; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-139-802-2

Query Match 70.2%; Score 40; DB 3; Length 13;

Best Local Similarity 66.7%; Pred. No. 8.2;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy

1 CPRECECIC 9

|||:|:|

Db 5 CPRLCQSC 13

RESULT 2

US-09-659-786-2

; Sequence 2, Application US/09659786

; Patent No. 6491894

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing

; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: P-LJ 3203

; CURRENT APPLICATION NUMBER: US/09/659,786

; CURRENT FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-659-786-2

Query Match 70.2%; Score 40; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
||| |||
Db 5 CPRLCQSSC 13

RESULT 3

US-08-926-914-2
; Sequence 2, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-926-914-2

Query Match 70.2%; Score 40; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
||| |||
Db 5 CPRLCQSSC 13

RESULT 4

US-09-428-082B-1071
; Sequence 1071, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-428-082B-1071

Query Match 70.2%; Score 40; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
||| |||
Db 5 CPRLCQSSC 13

RESULT 5

US-09-270-767-57784
; Sequence 57784, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57784
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57784

Query Match 70.2%; Score 40; DB 4; Length 58;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
||| |||
Db 39 CPREFEPVC 47

RESULT 6

US-09-270-767-42488
; Sequence 42488, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42488
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42488

Query Match      70.2%; Score 40; DB 4; Length 118;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CPRECECIC 9
      ||||| | : |
Db      39 CPREPEPVC 47

RESULT 7
US-09-252-991A-26031
; Sequence 26031, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26031
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26031

Query Match      70.2%; Score 40; DB 4; Length 596;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PRECECIC 9
      ||| : |||
Db      11 PRDCSSIC 18

RESULT 8
US-08-820-170A-37
; Sequence 37, Application US/08820170A
; Patent No. 5831058
; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Takeshi, WATANABE
; APPLICANT: Masato, HORIE
; APPLICANT: Toyomasa, KATAGIRI
; TITLE OF INVENTION: HUMAN GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,170A
; FILING DATE:

US-08-820-170A-37
; Sequence 37, Application US/09055699
; Patent No. 6005088
; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Takeshi, WATANABE
; APPLICANT: Masato, HORIE
; APPLICANT: Toyomasa, KATAGIRI
; TITLE OF INVENTION: HUMAN GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,699
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,170
; FILING DATE:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-055-699-37

Query Match      70.2%; Score 40; DB 3; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CPRECECIC 9
      | : ||| : |||
Db      326 CCKECKSIC 334

US-08-820-170A-37
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-170A-37

Query Match      70.2%; Score 40; DB 2; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CPRECECIC 9
      | : ||| : |||
Db      326 CCKECKSIC 334
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RESULT 10
US-09-273-565-37
; Sequence 37, Application US/09273565A
; Patent No. 6166190
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/273,565A
; CURRENT FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: 09/055,699
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: 08/820,170
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: JP 63410/1996
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: JP 69163/1997
; EARLIER FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-273-565-37

Query Match      70.2%; Score 40; DB 3; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CPRECESIC 9
      | :||:|
Db      326 CCKECKSIC 334

RESULT 11
US-09-565-538-37
; Sequence 37, Application US/09565538
; Patent No. 6333404
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/565,538
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/273,565
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-538-37

Query Match      70.2%; Score 40; DB 3; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CPRECESIC 9
      | :||:|
Db      326 CCKECKSIC 334

RESULT 12
US-09-661-468-37
; Sequence 37, Application US/09661468
; Patent No. 6376189
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/661,468
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-468-37

Query Match      70.2%; Score 40; DB 3; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CPRECESIC 9
      | :||:|
Db      326 CCKECKSIC 334

RESULT 13
US-09-976-165-37
; Sequence 37, Application US/09976165
; Patent No. 6562947
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/976,165
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/565,538
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-165-37

Query Match      70.2%; Score 40; DB 3; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Query Match 70.2%; Score 40; DB 4; Length 816;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECESIC 9
Db 326 CCKECSIC 334

RESULT 14
US-09-538-092-995
; Sequence 995, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 995
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number P23327
US-09-538-092-995

Query Match 68.4%; Score 39; DB 4; Length 699;
Best Local Similarity 55.6%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPRECESIC 9
Db 665 CPLVCETVC 673

RESULT 15
US-09-543-681A-5457
; Sequence 5457, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5457
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5457

Query Match 68.4%; Score 39; DB 4; Length 723;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPRECESIC 9
Db 141 CPRNLEAIC 149

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OM protein - protein search, using sw model

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75.615 Million cell updates/sec

Title: US-10-784-537-2

Perfect score: 57

Sequence: 1 CPRECECIC 9

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	9	16	US-10-363-204-123
2	50	87.7	13	16	US-10-363-204-127
3	47	82.5	31	16	US-10-363-204-125
4	44	77.2	58	14	US-10-106-698-5476
5	43	75.4	89	14	US-10-043-487-521
6	41	71.9	102	15	US-10-424-599-206937
7	40	70.2	13	9	US-09-765-086-2
8	40	70.2	13	9	US-09-840-277-32
9	40	70.2	13	14	US-10-264-374-2
10	40	70.2	13	14	US-10-375-992-2
11	40	70.2	13	15	US-10-609-217-1071
12	40	70.2	13	15	US-10-632-388-1071
13	40	70.2	13	15	US-10-651-723-1071

14	40	70.2	13	15	US-10-645-761-1071	Sequence 1071, Ap
15	40	70.2	13	15	US-10-666-696-1071	Sequence 1071, Ap
16	40	70.2	13	15	US-10-653-048-1071	Sequence 1071, Ap
17	40	70.2	13	15	US-10-264-374-2	Sequence 2, Appli
18	40	70.2	13	16	US-10-375-992-2	Sequence 2, Appli
19	40	70.2	59	17	US-10-425-115-220960	Sequence 220960,
20	40	70.2	63	10	US-09-948-783-122	Sequence 122, App
21	40	70.2	64	10	US-09-892-877-121	Sequence 121, App
22	40	70.2	77	17	US-10-425-115-364176	Sequence 364176,
23	40	70.2	136	14	US-10-263-828-79	Sequence 79, Appl
24	40	70.2	174	15	US-10-112-944-828	Sequence 828, App
25	40	70.2	230	15	US-10-112-944-375	Sequence 375, App
26	40	70.2	370	9	US-09-764-868-764	Sequence 764, App
27	40	70.2	387	15	US-10-168-618A-2	Sequence 2, Appli
28	40	70.2	481	9	US-09-815-242-5569	Sequence 5569, Ap
29	40	70.2	486	14	US-10-156-761-13717	Sequence 13717, A
30	40	70.2	487	9	US-09-815-242-12163	Sequence 12163, A
31	40	70.2	487	15	US-10-282-132A-44382	Sequence 44382, A
32	40	70.2	488	15	US-10-282-132A-63642	Sequence 63642, A
33	40	70.2	678	10	US-09-901-136-4	Sequence 4, Appli
34	40	70.2	682	10	US-09-901-136-2	Sequence 2, Appli
35	40	70.2	724	15	US-10-108-260A-3263	Sequence 3263, Ap
36	40	70.2	816	9	US-09-976-165-37	Sequence 37, Appl
37	40	70.2	816	14	US-10-342-276-37	Sequence 37, Appl
38	40	70.2	19608	15	US-10-084-846A-8	Sequence 8, Appli
39	39	68.4	100	17	US-10-425-115-300117	Sequence 300117,
40	39	68.4	123	15	US-10-424-599-168031	Sequence 168031,
41	39	68.4	445	15	US-10-424-599-170547	Sequence 170547,
42	39	68.4	699	14	US-10-369-493-21251	Sequence 21251, A
43	39	68.4	699	16	US-10-408-765A-434	Sequence 434, App
44	39	68.4	709	14	US-10-369-493-346	Sequence 346, App
45	38	66.7	13	9	US-09-765-086-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-363-204-123
; Sequence 123, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-204-123

Query Match 100.0%; Score 57; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9

Db 1 CPRECECIC 9

|||||||

RESULT 2

US-10-363-204-127
; Sequence 127, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:

; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127

Query Match 87.7%; Score 50; DB 16; Length 13;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRECESNC 13
|||||||

RESULT 3

US-10-363-204-125
; Sequence 125, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(31)
; OTHER INFORMATION: synthetic construct
US-10-363-204-125

Query Match 82.5%; Score 47; DB 16; Length 31;
Best Local Similarity 88.9%; Pred. No. 5,6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CIRECECIC 13
|||||||

RESULT 4

US-10-106-698-5476
; Sequence 5476, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5476
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5476

Query Match 77.2%; Score 44; DB 14; Length 58;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 29 CPRECSFLC 37
|||||

RESULT 5

US-10-043-487-521
; Sequence 521, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptide
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 521
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-521

Query Match 75.4%; Score 43; DB 14; Length 89;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PRECECIC 9
Db 23 PRECEPIC 30
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RESULT 6

US-10-424-599-206937
; Sequence 206937, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206937
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(102)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28891C.1.pap

US-10-424-599-206937

Query Match 71.9%; Score 41; DB 15; Length 102;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
| : | : | : |
Db 49 CTRDCEXVC 57

RESULT 7

US-09-765-086-2
; Sequence 2, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadhwani, Arup
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-2

Query Match 70.2%; Score 40; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
| : | : | : |
Db 5 CPRLCQSSC 13

RESULT 8

US-09-840-277-32
; Sequence 32, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-32

Query Match 70.2%; Score 40; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
| : | : | : |
Db 5 CPRLCQSSC 13

RESULT 9

US-10-264-374-2
; Sequence 2, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-2

Query Match 70.2%; Score 40; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECESIC 9
| : | : | : |
Db 5 CPRLCQSSC 13

RESULT 10

US-10-375-992-2
; Sequence 2, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; FILE REFERENCE: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,992

; FILING DATE: 27-Feb-2003
; CLASSIFICATION: 435
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-375-992-2

Query Match 70.2%; Score 40; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
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Db 5 CPRLCQSSC 13

RESULT 11
US-10-609-217-1071
; Sequence 1071, Application US/10609217
; Publication No. US2004004188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-1071

Query Match 70.2%; Score 40; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
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Db 5 CPRLCQSSC 13

RESULT 12
US-10-632-388-1071
; Sequence 1071, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA

; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-1071

Query Match 70.2%; Score 40; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
||| |:
Db 5 CPRLCQSSC 13

RESULT 13
US-10-651-723-1071
; Sequence 1071, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-651-723-1071

Query Match 70.2%; Score 40; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
||| |:
Db 5 CPRLCQSSC 13

RESULT 14
US-10-645-761-1071
; Sequence 1071, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.

; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-1071

Query Match 70.2%; Score 40; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRLCQSSC 13

RESULT 15
US-10-666-696-1071
; Sequence 1071, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGES, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1071
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-666-696-1071

Query Match 70.2%; Score 40; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRLCQSSC 13

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Job time : 44.1132 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:19:17 ; Search time 146.887 Seconds
(without alignments)
67.889 Million cell updates/sec

Title: US-10-784-537-2

Perfect score: 57

Sequence: 1 CPRECECIC 9

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- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
- 6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
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- 8: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
- 9: /cgn2_6/ptodata/1/paa/US085 COMB.pcp.*
- 10: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
- 11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
- 12: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
- 13: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
- 14: /cgn2_6/ptodata/1/paa/US090 COMB.pcp.*
- 15: /cgn2_6/ptodata/1/paa/US091 COMB.pcp.*
- 16: /cgn2_6/ptodata/1/paa/US092 COMB.pcp.*
- 17: /cgn2_6/ptodata/1/paa/US093 COMB.pcp.*
- 18: /cgn2_6/ptodata/1/paa/US094 COMB.pcp.*
- 19: /cgn2_6/ptodata/1/paa/US095 COMB.pcp.*
- 20: /cgn2_6/ptodata/1/paa/US096 COMB.pcp.*
- 21: /cgn2_6/ptodata/1/paa/US097 COMB.pcp.*
- 22: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
- 23: /cgn2_6/ptodata/1/paa/US099 COMB.pcp.*
- 24: /cgn2_6/ptodata/1/paa/US099A COMB.pcp.*
- 25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
- 26: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
- 27: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
- 28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
- 29: /cgn2_6/ptodata/1/paa/US103 COMB.pcp.*
- 30: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
- 31: /cgn2_6/ptodata/1/paa/US105 COMB.pcp.*
- 32: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*
- 33: /cgn2_6/ptodata/1/paa/US107 COMB.pcp.*
- 34: /cgn2_6/ptodata/1/paa/US108 COMB.pcp.*
- 35: /cgn2_6/ptodata/1/paa/US109 COMB.pcp.*
- 36: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Match	Length	DB	ID	Description
1	57	100.0	9	1	PCT-US01-27692A-123	Sequence 123, App
2	57	100.0	9	1	PCT-US02-27836-56	Sequence 56, Appl
3	57	100.0	9	29	US-10-363-204-123	Sequence 123, App
4	57	100.0	9	33	US-10-784-537-2	Sequence 2, Appli
5	50	87.7	13	1	PCT-US01-27692A-127	Sequence 127, App
6	50	87.7	13	1	PCT-US02-27836-60	Sequence 60, Appl
7	50	87.7	13	29	US-10-363-204-127	Sequence 127, App
8	50	87.7	13	33	US-10-784-537-3	Sequence 3, Appli
9	47	82.5	31	1	PCT-US01-27692A-125	Sequence 125, App
10	47	82.5	31	1	PCT-US02-27836-58	Sequence 58, Appl
11	47	82.5	31	29	US-10-363-204-125	Sequence 125, App
12	47	82.5	31	33	US-10-784-537-1	Sequence 1, Appli
13	47	82.5	31	33	US-10-784-537-5	Sequence 9, Appli
14	47	77.2	7	33	US-10-784-537-5	Sequence 5, Appli
15	44	77.2	8	33	US-10-784-537-6	Sequence 6, Appli
16	44	77.2	58	1	PCT-US00-26524B-5466	Sequence 5466, Ap
17	44	77.2	58	27	US-10-106-698-5476	Sequence 5476, Ap
18	43	75.4	89	26	US-10-043-487-521	Sequence 521, App
19	43	75.4	460	18	US-09-488-725A-1885	Sequence 1885, Ap
20	43	75.4	460	28	US-10-258-898A-1885	Sequence 1885, Ap
21	43	75.4	460	28	US-10-286-897-1885	Sequence 1885, Ap
22	43	75.4	512	18	US-09-488-725A-5457	Sequence 5457, Ap
23	43	75.4	512	28	US-10-258-898A-5457	Sequence 5457, Ap
24	43	75.4	512	28	US-10-286-897-5457	Sequence 5457, Ap
25	41	71.9	82	22	US-09-758-439-1223	Sequence 1223, Ap
26	41	71.9	82	28	US-10-201-915-1223	Sequence 1223, Ap
27	41	71.9	98	28	US-10-221-279-12244	Sequence 12244, A
28	41	71.9	102	30	US-10-424-599-206937	Sequence 206937, A
29	41	71.9	159	1	PCT-US99-22853B-1877	Sequence 1877, Ap
30	41	71.9	171	1	PCT-US99-22853B-1876	Sequence 1876, Ap
31	41	71.9	181	21	US-09-724-676-88311	Sequence 88311, A
32	41	71.9	181	21	US-09-724-676-88311	Sequence 88311, A
33	41	71.9	181	21	US-09-724-676-88311	Sequence 88311, A
34	41	71.9	181	21	US-09-724-676A-88324	Sequence 88324, A
35	41	71.9	181	27	US-10-170-205E-30329	Sequence 30329, A
36	41	71.9	191	1	PCT-US99-22853B-1875	Sequence 1875, Ap
37	41	71.9	399	36	US-60-550-051-290	Sequence 290, App
38	41	71.9	649	36	US-60-581-351-5898	Sequence 5898, Ap
39	40	70.2	13	1	PCT-US00-01602-2	Sequence 2, Appli
40	40	70.2	13	1	PCT-US99-25044-1027	Sequence 1027, Ap
41	40	70.2	13	1	PCT-US99-25044-1071	Sequence 1071, Ap
42	40	70.2	13	11	US-08-710-067-5	Sequence 5, Appli
43	40	70.2	13	16	US-09-235-902-2	Sequence 2, Appli
44	40	70.2	13	18	US-09-489-582-2	Sequence 2, Appli
45	40	70.2	13	19	US-09-563-286B-1071	Sequence 1071, Ap

ALIGNMENTS

RESULT 1
PCT-US01-27692A-123
; Sequence 123, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-123

Query Match 100.0%; Score 57; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | | |
Db 1 CPRECECIC 9

RESULT 2
PCT-US02-27836-56
; Sequence 56, Application PC/TUS0227836
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System (applicant for the
; APPLICANT: purposes of all designated states except US)
; APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of
; APPLICANT: America only)
; APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
; APPLICANT: only)
; APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of
; APPLICANT: America only)
; TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
; TITLE OF INVENTION: and Adipose Tissues
; FILE REFERENCE: 5774.P009PCT
; CURRENT APPLICATION NUMBER: PCT/US02/27836
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US02-27836-56

Query Match 100.0%; Score 57; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | | |
Db 1 CPRECECIC 9

RESULT 3
US-10-363-204-123
; Sequence 123, Application US/10363204
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-204-123

Query Match 100.0%; Score 57; DB 29; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | | |
Db 1 CPRECECIC 9

RESULT 4
US-10-784-537-2
; Sequence 2, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-784-537-2

Query Match 100.0%; Score 57; DB 33; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | | |
Db 1 CPRECECIC 9

RESULT 5
PCT-US01-27692A-127
; Sequence 127, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-127

Query Match 87.7%; Score 50; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRECESNC 13

RESULT 6
PCT-US02-27836-60
; Sequence 60, Application PC/TUS0227836
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System (applicant for the
; APPLICANT: purposes of all designated states except US)
; APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of
; APPLICANT: America only)
; APPLICANT: Arap, Wadiah (applicant for the purpose of the United States of America
; APPLICANT: only)
; APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of
; APPLICANT: America only)
; TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
; TITLE OF INVENTION: and Adipose Tissues
; FILE REFERENCE: 5774.P009PCT
; CURRENT APPLICATION NUMBER: PCT/US02/27836
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US02-27836-60

Query Match 87.7%; Score 50; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRECESNC 13

RESULT 7
US-10-363-204-127
; Sequence 127, Application US/10363204
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127

Query Match 87.7%; Score 50; DB 29; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRECESNC 13

RESULT 8
US-10-784-537-3
; Sequence 3, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIAH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-784-537-3

Query Match 87.7%; Score 50; DB 33; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRECESNC 13

RESULT 9
PCT-US01-27692A-125
; Sequence 125, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(31)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-125

Query Match 82.5%; Score 47; DB 1; Length 31;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
Db 5 CPRECESNC 13

RESULT 10
PCT-US02-27836-58
; Sequence 58, Application PC/TUS0227836
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System (applicant for the
; purposes of all designated states except US)
; APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of
; America only)
; APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
; only)
; APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of
; America only)
; TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
; FILE REFERENCE: 5774.P009PCT
; CURRENT APPLICATION NUMBER: PCT/US02/27836
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US02-27836-58

Query Match 82.5%; Score 47; DB 1; Length 31;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | |
Db 5 CIRECESIC 13

RESULT 11
US-10-363-204-125
; Sequence 125, Application US/10363204
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(31)
; OTHER INFORMATION: synthetic construct
US-10-363-204-125

Query Match 82.5%; Score 47; DB 29; Length 31;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | |
Db 5 CIRECESIC 13

RESULT 12
US-10-784-537-1
; Sequence 1, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIH

; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-784-537-1

Query Match 82.5%; Score 47; DB 33; Length 31;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECECIC 9
| | | | | | | |
Db 5 CIRECESIC 13

RESULT 13
US-10-784-537-9
; Sequence 9, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-784-537-9

Query Match 82.5%; Score 47; DB 33; Length 31;

Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPRECES 9
Db 5 CIRECESIC 13

RESULT 14

US-10-784-537-5

; Sequence 5, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-10-784-537-5

Query Match 77.2%; Score 44; DB 33; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPRECES 7
Db 1 CPRECES 7

RESULT 15

US-10-784-537-6

; Sequence 6, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266

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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:24:42 ; Search time 4.07547 Seconds
(without alignments)
40.083 Million cell updates/sec

Title: US-10-784-537-2

Perfect score: 57

Sequence: 1 CPRECECIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 80665 seqs, 18150633 residues

Total number of hits satisfying chosen parameters: 80665

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	9	6 US-10-489-071-56	Sequence 56, Appl
2	50	87.7	13	6 US-10-489-071-60	Sequence 60, Appl
3	47	82.5	31	6 US-10-489-071-58	Sequence 58, Appl
4	38	66.7	143	6 US-10-220-366A-18045	Sequence 18045, A
5	37	64.9	388	6 US-10-220-366A-26731	Sequence 26731, A
6	37	64.9	417	5 US-09-993-2348-6	Sequence 6, Appl
7	37	64.9	844	6 US-10-411-9108-48	Sequence 48, Appl
8	37	64.9	2471	6 US-10-765-727-23	Sequence 23, Appl
9	37	64.9	2471	6 US-10-846-989-57	Sequence 57, Appl
10	36	63.2	80	6 US-10-976-102-78	Sequence 78, Appl
11	36	63.2	80	6 US-10-976-102-79	Sequence 79, Appl
12	36	63.2	80	6 US-10-976-102-96	Sequence 96, Appl
13	35	61.4	64	6 US-10-220-366A-22211	Sequence 22211, A
14	35	61.4	80	6 US-10-976-102-89	Sequence 89, Appl
15	35	61.4	102	6 US-10-220-366A-17365	Sequence 17365, A
16	35	61.4	102	6 US-10-220-366A-24597	Sequence 24597, A
17	35	61.4	1047	6 US-10-468-026-2	Sequence 2, Appl
18	35	61.4	2768	6 US-10-510-101-72	Sequence 72, Appl
19	34	59.6	13	1 PCT-US04-34918-38	Sequence 38, Appl
20	34	59.6	13	6 US-10-970-847-38	Sequence 38, Appl
21	34	59.6	225	6 US-10-950-374-497	Sequence 497, Appl
22	34	59.6	225	6 US-10-955-952-282	Sequence 282, Appl
23	34	59.6	225	6 US-10-157-779-282	Sequence 282, Appl
24	34	59.6	225	6 US-10-964-241-282	Sequence 282, Appl
25	34	59.6	291	6 US-10-732-923-14208	Sequence 14208, A

RESULT 1
US-10-489-071-56
; Sequence 56, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUAINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-56

Query Match 100.0%; Score 57; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
DB 1 CPRECECIC 9

RESULT 2
US-10-489-071-60
; Sequence 60, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUAINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60
; LENGTH: 13
; TYPE: PRT

26 34 59.6 365 6 US-10-732-923-16980 Sequence 16980, A
27 34 59.6 818 6 US-10-732-923-14186 Sequence 14186, A
28 34 59.6 818 6 US-10-732-923-14187 Sequence 14187, A
29 34 59.6 833 6 US-10-732-923-14221 Sequence 14221, A
30 34 59.6 1024 6 US-10-732-923-14220 Sequence 14220, A
31 34 59.6 1104 6 US-10-732-923-14222 Sequence 14222, A
32 34 59.6 1114 6 US-10-732-923-14185 Sequence 14185, A
33 34 59.6 1119 6 US-10-732-923-14213 Sequence 14213, A
34 34 59.6 1120 6 US-10-732-923-14219 Sequence 14219, A
35 34 59.6 1624 6 US-10-363-374-6 Sequence 6, Appli
36 33 57.9 13 1 PCT-US04-34918-19 Sequence 19, Appl
37 33 57.9 13 6 US-10-970-847-19 Sequence 19, Appl
38 33 57.9 54 6 US-10-951-866-15 Sequence 15, Appl
39 33 57.9 80 6 US-10-976-102-70 Sequence 70, Appl
40 33 57.9 81 6 US-10-732-923-3520 Sequence 3520, Ap
41 33 57.9 149 6 US-10-220-366A-18544 Sequence 18544, A
42 33 57.9 184 6 US-10-220-366A-14624 Sequence 14624, A
43 33 57.9 383 5 US-09-963-693B-105 Sequence 105, App
44 33 57.9 421 6 US-10-735-256-9 Sequence 9, Appli
45 33 57.9 461 6 US-10-735-256-4 Sequence 4, Appli

ALIGNMENTS

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-60

Query Match      87.7%; Score 50; DB 6; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.024; 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 CPRECECIC 9
Db 5 CPRECESNC 13

RESULT 3
US-10-489-071-58
; Sequence 58, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUALINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; FILE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-58

Query Match      82.5%; Score 47; DB 6; Length 31;
Best Local Similarity 88.9%; Pred. No. 0.15; 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
Db 5 CIRECECIC 13

RESULT 4
US-10-220-366A-18045
; Sequence 18045, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 18045
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(143)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-18045

Query Match      66.7%; Score 38; DB 6; Length 143;
Best Local Similarity 55.6%; Pred. No. 14; 2; Indels 2; Gaps 0;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CPRECECIC 9
Db 53 CARQCVSVC 61

RESULT 5
US-10-220-366A-26731
; Sequence 26731, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 26731
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(388)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-26731

Query Match      64.9%; Score 37; DB 6; Length 388;
Best Local Similarity 55.6%; Pred. No. 51; 3; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
Db 102 CDRCEPLC 110

RESULT 6
US-09-993-234B-6
; Sequence 6, Application US/09993234B
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/09/993,234B
; FILING DATE: 19-Nov-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828683
; FILING DATE: 31-MAR-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
```

```
; REFERENCE/DOCKET NUMBER: P1007PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-993-234B-6

Query Match      64.9%; Score 37; DB 5; Length 417;
Best Local Similarity 44.4%; Pred. No. 54;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPRECESIC 9
Db      187 CPERCAVC 195

RESULT 7
US-10-411-910B-48
; GENERAL INFORMATION:
; APPLICANT: DILLON, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910B
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Desulfitobacterium hafnienae
US-10-411-910B-48

Query Match      64.9%; Score 37; DB 6; Length 844;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPRECESIC 9
Db      181 CPHSCEAQC 189

RESULT 8
US-10-765-727-23
; Sequence 23, Application US/10765727
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
; FILE REFERENCE: 674525-2010
; CURRENT APPLICATION NUMBER: US/10/765,727
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03426
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: GB 0118153.6
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: GB 0207930.9
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB 0212282.8
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: GB 0212283.6
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 2471

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-765-727-23

Query Match      64.9%; Score 37; DB 6; Length 2471;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 PRECESIC 9
Db      1371 PRDCESGC 1378

RESULT 9
US-10-846-989-57
; Sequence 57, Application US/10846989
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: RAGNO, SILVIA
; APPLICANT: TUGAL, TAMARA
; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MEDICAL TREATMENT
; FILE REFERENCE: 654525-2012
; CURRENT APPLICATION NUMBER: US/10/846,989
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0127271.5
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 57
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-846-989-57

Query Match      64.9%; Score 37; DB 6; Length 2471;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 PRECESIC 9
Db      1371 PRDCESGC 1378

RESULT 10
US-10-976-102-78
; Sequence 78, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
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US-10-976-102-78

Query Match 63.2%; Score 36; DB 6; Length 80;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
DB 48 CPSECDRRC 56

RESULT 11

US-10-976-102-79
; Sequence 79, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-976-102-79

Query Match 63.2%; Score 36; DB 6; Length 80;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
DB 48 CPSECDRRC 56

RESULT 12

US-10-976-102-96
; Sequence 96, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-976-102-96

Query Match 63.2%; Score 36; DB 6; Length 80;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
DB 48 CPSECDRRC 56

RESULT 13

US-10-220-366A-22211
; Sequence 22211, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 22211
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(64)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-22211

Query Match 61.4%; Score 35; DB 6; Length 64;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
DB 9 CVRVCEVC 17

RESULT 14

US-10-976-102-89
; Sequence 89, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-976-102-89

Query Match 61.4%; Score 35; DB 6; Length 80;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
DB 45 CPKACEYRC 53

RESULT 15

US-10-220-366A-17365
; Sequence 17365, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC

; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 17365
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(102)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-17365

Query Match 61.4%; Score 35; DB 6; Length 102;
Best Local Similarity 44.4%; Pred. NO. 30;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
| : : : :
Db 60 CAHDCDNC 68

Search completed: November 16, 2004, 14:47:12
Job time : 4.07547 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:15:03 ; Search time 10.1887 Seconds
(without alignments)
84.991 Million cell updates/sec

Title: US-10-784-537-2

Perfect score: 57

Sequence: 1 CPRECECIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	82.5	425	2 AE2094	hypothetical prote
2	41	71.9	273	2 T16246	hypothetical prote
3	40	70.2	395	2 S75552	hypothetical prote
4	40	70.2	487	2 T34868	probable glutamate
5	40	70.2	487	2 B89813	NADH-glutamate syn
6	40	70.2	488	2 F86916	NADH-dependent glu
7	40	70.2	835	2 JP0076	nel protein - chic
8	40	70.2	3133	2 S52093	hemocytin - silkw
9	39	68.4	211	1 WBEEMA	23.5K protein - Ma
10	39	68.4	211	1 WBEEMB	23.5K protein - Ma
11	39	68.4	358	2 T23802	hypothetical prote
12	39	68.4	699	2 A54660	histidine rich cal
13	39	68.4	852	2 A34373	histidine-rich cal
14	38	66.7	372	2 T23680	hypothetical prote
15	38	66.7	708	2 A83407	formate dehydrogen
16	38	66.7	743	2 B97498	molybdopter in oxid
17	38	66.7	743	2 AG2716	reductase [importe
18	38	66.7	2219	2 T27684	hypothetical prote
19	37.5	65.8	290	2 G72858	Acorf-70 protein -
20	37	64.9	209	2 F64416	polyferredoxin - M
21	37	64.9	457	2 T03449	protein V - Hendra
22	37	64.9	474	2 E75069	glutamate synthase
23	37	64.9	475	2 B75024	glutamate synthase
24	37	64.9	488	2 B75551	glutamate synthase
25	37	64.9	489	2 F82085	glutamate synthase
26	37	64.9	554	2 T25288	hypothetical prote
27	37	64.9	573	2 JC4335	anti-mullerian hor
28	37	64.9	859	2 S69700	hypothetical prote
29	37	64.9	888	2 H88085	protein Tlfl.8 [i

30	37	64.9	1353	2 T19691	hypothetical prote
31	37	64.9	2109	2 I38414	transcription fact
32	36	63.2	106	2 T49958	GASA4 - Arabidopsi
33	36	63.2	106	2 S60232	gibberellin-regula
34	36	63.2	159	2 C81662	cytosolic acyl-CoA
35	36	63.2	160	2 F71502	probable acyl-coa
36	36	63.2	413	2 T32691	hypothetical prote
37	36	63.2	484	2 G98262	glutamate synthase
38	36	63.2	484	2 AC3022	glutamate synthase
39	36	63.2	499	2 AE3514	glutamate synthase
40	36	63.2	522	2 H86248	protein T23J18.22
41	36	63.2	539	2 T46720	hypothetical prote
42	36	63.2	567	2 T15574	hypothetical prote
43	36	63.2	575	1 HNN239	hemagglutinin-neur
44	36	63.2	575	2 A43487	hemagglutinin-neur
45	36	63.2	667	2 S64915	EMP70 protein prec

ALIGNMENTS

RESULT 1

AE2094

hypothetical protein alr2308 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AE2094

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2094

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-425 <KUR>

A:Cross-references: UNIPROT:Q8YUN1; GB:BA000019; PIDN:BAB74007.1; PID:g17131400; GSPDB:GN

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr2308

Query Match 82.5%; Score 47; DB 2; Length 425;

Best Local Similarity 77.8%; Pred. NO. 5.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPRECECIC 9

DB 112 CPRPCEKIC 120

RESULT 2

T16246

hypothetical protein F35A5.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16246

R:Leimbach, D.

submitted to the EMBL Data Library, January 1996

A:Description: The sequence of C. elegans cosmid F35A5.

A:Reference number: Z18485

A:Accession: T16246

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-273 <LEI>

A:Cross-references: UNIPROT:Q20000; EMBL:U46675; MID:g1166613; PID:g1166614; PIDN:AAB5261

A:Experimental source: strain Bristol N2; clone F35A5

C:Genetics:

A:Gene: CESP:F35A5.4

A:Map position: X

A:Introns: 18/3; 62/3; 81/3; 100/3; 140/3; 226/2

Query Match 71.9%; Score 41; DB 2; Length 273;

Best Local Similarity 44.4%; Pred. No. 31;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
|||:|:|
DB 146 CPQQCQPCVC 154

RESULT 3
S75952
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75952
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75952
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-395 <XAN>
A;Cross-references: UNIPROT:Q55456; EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAA1079
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG

Query Match 70.2%; Score 40; DB 2; Length 395;
Best Local Similarity 55.6%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
|||:|:|
DB 131 CPRPCAQVC 139

RESULT 4
T34868
probable glutamate synthase small chain - *Streptomyces coelicolor*
C;Species: *Streptomyces coelicolor*
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34868
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21560
A;Accession: T34868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-487 <SEE>
A;Cross-references: UNIPROT:Q9S220; EMBL:AL109849; PIDN:CAB52860.1; GSFDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: gltD; SCOE:SC3A3.03c
C;Superfamily: glutamate synthase small chain

Query Match 70.2%; Score 40; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPRECECIC 9
|||:|:|
DB 98 CPAPCESAC 106

RESULT 5
B89813
NADH-glutamate synthase small subunit gltD [imported] - *Staphylococcus aureus* (strain N
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004
C;Accession: B89813

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-487 <KUR>
A:Cross-references: UNIPROT:Q99WD0; GB:BA000018; PID:gl3700363; PIDN:BA041661.1; GSPDB:GN
A:Experimental source: strain N315
C:Genetics:
A:Gene: gldD
C:Superfamily: Glutamate synthase, small subunit

Query Match 70.2%; Score 40; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPRECECIS 9
Db 106 CPAPCESAC 114

RESULT 6
F86916
NADH-dependent glutamate synthase small subunit gldD [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
C:Accession: F86916
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hori, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: F86916
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-488 <STO>
A:Cross-references: UNIPROT:Q9CDD4; GB:AL450380; NID:gl3092455; PIDN:CAC29570.1; GSPDB:GN
C:Genetics:
A:Gene: gldD
C:Superfamily: Glutamate synthase, small subunit

Query Match 70.2%; Score 40; DB 2; Length 488;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPRECECIS 9
Db 98 CPAPCESAC 106

RESULT 7
JP0076
nel protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 04-Apr-2004
C:Accession: A38963; JP0076
R;Matsushashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K. Dev. Dyn. 203, 212-222, 1995
A:Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expressed in the developing chick embryo.
A:Reference number: A38963; MUID:95383734; PMID:7655083
A:Accession: A38963
A:Molecule type: mRNA
A:Residues: 1-835 <MAT>
A:Cross-references: DDBJ:D45365
A:Experimental source: 9-day embryo
R;Matsushashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K. Submitted to JIPID, January 1995

Matches	5;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	CPRECESIC 9							
				:					
Db	162	CPRTCSVVC 170							
RESULT 10									
WMBEM									
23.5K protein - Marek's disease virus (type 1, strains Md5 and GA)									
N;Alternate names: UL45h protein									
C;Species: Marek's disease virus									
A;Note: host Gallus gallus (chicken)									
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999									
C;Accession: B22818; JQ2207									
R;Ihara, T.; Kato, A.; Ueda, S.; Ishihama, A.; Hirai, K.									
Virus Genes 3, 127-140, 1989									
A;Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene b									
A;Reference number: A22818; MUID:90142542; PMID:2559540									
A;Accession: B22818									
A;Molecule type: DNA									
A;Residues: 1-211 <IHA>									
A;Experimental source: strain Md5									
R;Yanagida, N.; Yoshida, S.; Nazerian, K.; Lee, L.F.									
J. Gen. Virol. 74, 1837-1845, 1993									
A;Title: Nucleotide and predicted amino acid sequences of Marek's disease virus									
A;Reference number: JQ2199; MUID:93389438; PMID:8397281									
A;Accession: JQ2207									
A;Molecule type: DNA									
A;Residues: 1-211 <YAN>									
A;Cross-references: GB:U10283; NID:g388703; PIDN:AAA03152.1; PID:g388710									
A;Experimental source: strain GA									
C;Superfamily: turkey herpesvirus 23.5K protein									
Query Match 68.4%; Score 39; DB 1; Length 211;									
Best Local Similarity 55.6%; Pred. No. 51;									
Matches	5;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	CPRECESIC 9							
				:					
Db	162	CPRTCSVVC 170							
RESULT 11									
T23802									
hypothetical protein M195.2 - Caenorhabditis elegans									
C;Species: Caenorhabditis elegans									
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004									
C;Accession: T23802									
R;Burton, J.									
submitted to the EMBL Data Library, October 1995									
A;Reference number: Z19801									
A;Accession: T23802									
A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Molecule type: DNA									
A;Residues: 1-358 <WIL>									
A;Cross-references: UNIPROT:Q21563; EMBL:Z66498; PIDN:CAA91291.1; GSPDB:GN00020									
A;Experimental source: clone M195									
C;Genetics:									
A;Gene: CESP:M195.2									
A;Map position: 2									
A;Introns: 90/3; 162/3; 207/3; 270/2									
C;Superfamily: gliadin									
Query Match 68.4%; Score 39; DB 2; Length 358;									
Best Local Similarity 55.6%; Pred. No. 74;									
Matches	5;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	CPRECESIC 9							
				:					
Db	271	CSSECQSVVC 279							

```
RESULT 12
A:AS4660
histidine rich calcium binding protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: AS4660
R:Hofmann, S.L.; Topham, M.; Hsieh, C.L.; Francke, U.
Genomics 9, 656-669, 1991
A:Title: cDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and localization of its gene
A:Reference number: AS4660; MUID:91244309; PMID:2037293
A:Accession: AS4660
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-699 <HOF>
A:Cross-references: UNIPROT:P23327; GB:M60052; NID:G183918; PIDN:AAA88071.1; PID:G183918
C:Genetics:
A:Gene: GDB:HRC
A:Cross-references: GDB:126369; OMIM:142705
A:Map position: 19q13.3-19q13.3
C:Keywords: calcium binding

Query Match      68.4%; Score 39; DB 2; Length 699;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CPRECECIC 9
      |||::|
Db      665 CPLVCETVC 673

RESULT 13
A:34373
histidine-rich calcium-binding protein precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34373
R:Hofmann, S.L.; Goldstein, J.L.; Orth, K.; Moomaw, C.R.; Slaughter, C.A.; Brown, M.S.
J. Biol. Chem. 264, 18083-18090, 1989
A:Title: Molecular cloning of a histidine-rich Ca(2+)-binding protein of sarcoplasmic reticulum
A:Reference number: A34373; MUID:90036884; PMID:2808365
A:Accession: A34373
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-852 <HOF>
A:Cross-references: UNIPROT:P16230; GB:J05080; NID:G165099; PIDN:AAA31279.1; PID:G165100
C:Keywords: calcium binding

Query Match      68.4%; Score 39; DB 2; Length 852;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CPRECECIC 9
      |||::|
Db      818 CPLVCETVC 826

RESULT 14
A:T23680
hypothetical protein M02G9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23680
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19781
A:Accession: T23680
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-372 <WIL>
A:Cross-references: UNIPROT:O17969; EMBL:Z81573; PIDN:CAB04624.1; GSPDB:GN00020; CESP:M02G9
A:Experimental source: clone M02G9
C:Genetics:
A:Gene: CESP:M02G9.2
```

```
A:Map position: 2
A:Introns: 17/3; 72/3; 181/3; 232/2; 258/3; 294/3; 336/1
C:Superfamily: gliadin

Query Match      66.7%; Score 38; DB 2; Length 372;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPRECECIC 9
      |||::|
Db      184 CPTECQPAC 192

RESULT 15
A:AE3407
formate dehydrogenase (EC 1.2.1.2) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AE3407
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3407
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-708 <KUR>
A:Cross-references: UNIPROT:Q8YGB6; GB:AE008917; PIDN:AAL52424.1; PID:G17983227; GSPDB:GN00020
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11243
A:Map position: 1
C:Superfamily: formate dehydrogenase
C:Keywords: oxidoreductase

Query Match      66.7%; Score 38; DB 2; Length 708;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPRECECIC 9
      |||::|
Db      17 CPDCCPSTC 25

Search completed: November 16, 2004, 14:30:51
Job time : 11.1887 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:09:48 ; Search time 176.642 Seconds
(without alignments)
62.956 Million cell updates/sec

Title: US-10-784-537-1

Perfect score: 198

Sequence: 1 CYNICRECSICGADGACWTWCADGCSRSC 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	31	5	ABG60450 Selective
2	198	100.0	31	6	ABR56862 Aminopept
3	73	36.9	2808	8	ADP31258 Human sec
4	73	36.9	4683	8	ADP31260 Human sec
5	73	36.9	4848	8	ADP31259 Human sec
6	71.5	36.1	2027	8	ADP31058 Human sec
7	71	35.9	291	8	ADP30639 Human sec
8	71	35.9	291	8	ADP30638 Human sec
9	71	35.9	291	8	ADP30636 Human sec
10	71	35.9	659	8	ADP30692 Human sec
11	71	35.9	659	8	ADP30720 Human sec
12	71	35.9	659	8	ADP30699 Human sec
13	71	35.9	659	8	ADP30701 Human sec
14	71	35.9	659	8	ADP30712 Human sec
15	71	35.9	659	8	ADP30722 Human sec
16	71	35.9	1478	8	ADP30565 Human sec
17	71	35.9	2803	8	ADP30749 Human sec
18	70.5	35.6	7285	6	ABJ38280 pAMC21-RA
19	70	35.4	291	8	ADP30630 Human sec
20	70	35.4	291	8	ADP30633 Human sec
21	70	35.4	375	8	ADP30606 Human sec
22	69.5	35.1	2700	8	ADP30910 Human sec
23	69.5	35.1	2700	8	ADP30911 Human sec
24	69	34.8	2827	8	ADP30681 Human sec
25	68	34.3	1001	8	ADP31356 Human sec

26	68	34.3	2124	8	ADP30560 Human sec
27	67	33.8	61	6	ABR55376 A polypep
28	67	33.8	61	6	ADL23896 Buchoid s
29	67	33.8	585	8	ADP31445 Human sec
30	67	33.8	711	8	ADP31215 Human sec
31	66.5	33.6	507	8	ADP30869 Human sec
32	66.5	33.6	2358	8	ADP31690 Human sec
33	66	33.3	930	8	ADP30949 Human sec
34	65.5	33.1	423	8	ADP31323 Human sec
35	65	32.8	444	8	ADP31478 Human sec
36	65	32.8	1044	8	ADP31550 Human sec
37	65	32.8	2272	8	ADP31136 Human sec
38	65	32.8	2542	8	ADP31594 Human sec
39	65	32.8	3036	8	ADP31595 Human sec
40	65	32.8	3585	8	ADP31117 Human sec
41	65	32.8	8973	8	ADP31119 Human sec
42	64.5	32.6	1227	8	ADP31210 Human sec
43	64.5	32.6	1344	8	ADP31211 Human sec
44	64.5	32.6	2858	4	ABB71150 Drosophil
45	64.5	32.6	3060	4	ABB58064 Drosophil

ALIGNMENTS

RESULT 1
ABG60450
ID ABG60450 standard; peptide; 31 AA.

XX AC ABG60450;

XX DT 30-JUL-2002 (first entry)

XX DE Selective targeting peptide #125.

XX KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
XX KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
XX KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
XX KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
XX KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
XX KW gene therapy.

XX OS Synthetic.

XX PN WO200220769-A1.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US027692.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Arap W, Pasqualini R;

XX DR WPI; 2002-415731/44.

XX KW Targeting peptides identified by phage display, useful for targeting
XX KW delivery to an organ or tissue, particularly for treating a disease, e.g.
XX KW cancer, inflammatory or autoimmune diseases, infections or cardiovascular
XX KW disease.

XX PS Claim 22; Page 108; 317pp; English.

XX CC The invention relates to an isolated peptide of 100 amino acids or less
XX CC in size useful for targeting delivery to an organ or tissue, particularly
XX CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
XX CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
XX CC infection, cardiovascular disease or degenerative disease. The peptide is
XX CC also useful for inducing apoptosis, particularly to a subject with
XX CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 09-JUN-2003; 2003US-047609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
DR WPI; 2004-348438/32.
XX
PT New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
PS Claim 1; SEQ ID NO 3256; 428pp; English.
XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPONEB and is not in the specification.
XX
SQ Sequence 2808 AA;

Query Match 36.9%; Score 73; DB 8; Length 2808;
Best Local Similarity 45.2%; Pred. No. 42;
Matches 14; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CYNLCIRCESICGADGACWTWCAGCSRSC 31
Db 1974 CTTCTGTGCCACGAGACCTGC--GCTTCC 202

RESULT 4
ID ADF31260 standard; protein; 4693 AA.
XX
AC ADF31260;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human secreted protein SEQ ID #2027.
XX
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX

OS Homo sapiens.
XX WO2004035732-A2.
PN
XX
PD
XX
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 09-JUN-2003; 2003US-047609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493341P.

CC treating diseases such as proliferative (e.g. cancer), inflammatory,
 CC immune, metabolic, genetic, bacterial and viral diseases. The present
 CC sequence represents a human secreted protein. The present sequence is
 CC available on WIPOWEB and is not in the specification.

SQ Sequence 4848 AA;

Query Match 36.9%; Score 73; DB 8; Length 4848;
 Best Local Similarity 45.2%; Pred. No. 67;
 Matches 14; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 1 CYNLCIRECESICGAGACWTWCADGCSRSC 31
 DB 2214 CTTTGTGTCACGAGACCTGTC--GCTTCC 2242

RESULT 6

ADP31058

ID ADP31058 standard; protein; 2027 AA.

XX ADP31058;

DT 12-AUG-2004 (first entry)

DE Human secreted protein SEQ ID #1825.

KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
 KW cancer; inflammatory; immune; human secreted protein.

OS Homo sapiens.

XX WO2004035732-A2.

XX 29-APR-2004.

XX 28-AUG-2003; 2003WO-US026780.

PR 29-AUG-2002; 2002US-0406576P.

PR 29-AUG-2002; 2002US-0406579P.

PR 29-AUG-2002; 2002US-0406585P.

PR 29-AUG-2002; 2002US-0406588P.

PR 29-AUG-2002; 2002US-0406608P.

PR 29-AUG-2002; 2002US-0406611P.

PR 29-AUG-2002; 2002US-0406612P.

PR 29-AUG-2002; 2002US-0406616P.

PR 29-AUG-2002; 2002US-0406640P.

PR 29-AUG-2002; 2002US-0406642P.

PR 29-AUG-2002; 2002US-0406646P.

PR 29-AUG-2002; 2002US-0406653P.

PR 29-AUG-2002; 2002US-0406655P.

PR 29-AUG-2002; 2002US-0406666P.

PR 17-SEP-2002; 2002US-0410946P.

PR 17-SEP-2002; 2002US-0410947P.

PR 17-SEP-2002; 2002US-0410948P.

PR 17-SEP-2002; 2002US-0410949P.

PR 17-SEP-2002; 2002US-0410953P.

PR 17-SEP-2002; 2002US-0410957P.

PR 17-SEP-2002; 2002US-0410958P.

PR 17-SEP-2002; 2002US-0410959P.

PR 17-SEP-2002; 2002US-0410960P.

PR 17-SEP-2002; 2002US-0410961P.

PR 17-SEP-2002; 2002US-0410962P.

PR 17-SEP-2002; 2002US-0411013P.

PR 17-SEP-2002; 2002US-0411022P.

PR 17-SEP-2002; 2002US-0411023P.

PR 17-SEP-2002; 2002US-0411024P.

PR 17-SEP-2002; 2002US-0411032P.

PR 17-SEP-2002; 2002US-0411035P.

PR 17-SEP-2002; 2002US-0411037P.

PR 17-SEP-2002; 2002US-0411041P.

PR 17-SEP-2002; 2002US-0411045P.

PR 17-SEP-2002; 2002US-0411046P.

PR 17-SEP-2002; 2002US-0411048P.

PR 17-SEP-2002; 2002US-0411052P.
 PR 17-SEP-2002; 2002US-0411055P.
 PR 17-SEP-2002; 2002US-0411073P.
 PR 17-SEP-2002; 2002US-0411082P.
 PR 17-SEP-2002; 2002US-0411101P.
 PR 17-SEP-2002; 2002US-0411111P.
 PR 18-APR-2003; 2003US-0463700P.
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 19-MAY-2003; 2003US-0471306P.
 PR 19-MAY-2003; 2003US-0471336P.
 PR 22-MAY-2003; 2003US-0472420P.
 PR 22-MAY-2003; 2003US-0472430P.
 PR 09-JUN-2003; 2003US-0476609P.
 PR 09-JUN-2003; 2003US-0476641P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 15-JUL-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;

XX Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;

XX Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

XX WPI; 2004-348438/32.

XX New nucleic acid molecule for diagnosing, preventing or treating diseases
 PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
 PT genetic, bacterial and viral diseases.

XX Claim 1; SEQ ID NO 3056; 428pp; English.

XX The present invention relates to an isolated nucleic acid molecule
 CC encoding a polypeptide which is believed to be cytostatic,
 CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
 CC composition and methods are useful for diagnosing, preventing and
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,
 CC immune, metabolic, genetic, bacterial and viral diseases. The present
 CC sequence represents a human secreted protein. The present sequence is
 CC available on WIPOWEB and is not in the specification.

SQ Sequence 2027 AA;

Query Match 36.1%; Score 71.5; DB 8; Length 2027;

Best Local Similarity 45.2%; Pred. No. 45;

Matches 14; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

QY 1 CYNLCIRECESICGAGACWTWCADGCSRSC 31

DB 887 CAACCTGTC-CCCGAGACCTACCGGCCTC 916

RESULT 7

ADP30639

ID ADP30639 standard; protein; 291 AA.

XX ADP30639;

XX ADP30639;

DT 12-AUG-2004 (first entry)
XX Human secreted protein SEQ ID #1406.
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX Homo sapiens.
XX WO2004035732-A2.
XX 29-APR-2004.
XX 28-AUG-2003; 2003WO-US026780.
XX 29-AUG-2002; 2002US-0406576P.
XX 29-AUG-2002; 2002US-0406579P.
XX 29-AUG-2002; 2002US-0406585P.
XX 29-AUG-2002; 2002US-0406588P.
XX 29-AUG-2002; 2002US-0406608P.
XX 29-AUG-2002; 2002US-0406611P.
XX 29-AUG-2002; 2002US-0406612P.
XX 29-AUG-2002; 2002US-0406616P.
XX 29-AUG-2002; 2002US-0406640P.
XX 29-AUG-2002; 2002US-0406642P.
XX 29-AUG-2002; 2002US-0406646P.
XX 29-AUG-2002; 2002US-0406653P.
XX 29-AUG-2002; 2002US-0406655P.
XX 29-AUG-2002; 2002US-0406666P.
XX 17-SEP-2002; 2002US-0410946P.
XX 17-SEP-2002; 2002US-0410947P.
XX 17-SEP-2002; 2002US-0410948P.
XX 17-SEP-2002; 2002US-0410949P.
XX 17-SEP-2002; 2002US-0410953P.
XX 17-SEP-2002; 2002US-0410957P.
XX 17-SEP-2002; 2002US-0410958P.
XX 17-SEP-2002; 2002US-0410959P.
XX 17-SEP-2002; 2002US-0410960P.
XX 17-SEP-2002; 2002US-0410961P.
XX 17-SEP-2002; 2002US-0410962P.
XX 17-SEP-2002; 2002US-0411019P.
XX 17-SEP-2002; 2002US-0411022P.
XX 17-SEP-2002; 2002US-0411023P.
XX 17-SEP-2002; 2002US-0411024P.
XX 17-SEP-2002; 2002US-0411032P.
XX 17-SEP-2002; 2002US-0411035P.
XX 17-SEP-2002; 2002US-0411037P.
XX 17-SEP-2002; 2002US-0411041P.
XX 17-SEP-2002; 2002US-0411045P.
XX 17-SEP-2002; 2002US-0411046P.
XX 17-SEP-2002; 2002US-0411048P.
XX 17-SEP-2002; 2002US-0411052P.
XX 17-SEP-2002; 2002US-0411055P.
XX 17-SEP-2002; 2002US-0411073P.
XX 17-SEP-2002; 2002US-0411082P.
XX 17-SEP-2002; 2002US-0411101P.
XX 17-SEP-2002; 2002US-0411111P.
XX 18-APR-2003; 2003US-0463700P.
XX 18-APR-2003; 2003US-0463708P.
XX 18-APR-2003; 2003US-0463716P.
XX 02-MAY-2003; 2003US-0467199P.
XX 02-MAY-2003; 2003US-0467201P.
XX 02-MAY-2003; 2003US-0467203P.
XX 19-MAY-2003; 2003US-0467230P.
XX 19-MAY-2003; 2003US-0471306P.
XX 19-MAY-2003; 2003US-0471336P.
XX 22-MAY-2003; 2003US-0472430P.
XX 09-JUN-2003; 2003US-0476609P.
XX 09-JUN-2003; 2003US-0476641P.
XX 08-JUL-2003; 2003US-0485218P.
XX 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RP, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX Claim 1; SEQ ID NO 2637; 428pp; English.
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX Sequence 291 AA;
SQ
Query Match 35.9%; Score 71; DB 8; Length 291;
Best Local Similarity 57.9%; Pred. No. 9.6;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 13 CGADGACWTWCADGCSRC 31
||| ||| ||| ||| : :
Db 230 CGAGGCCCTGCAGGCTTC 248
RESULT 8
ADP30638
ID ADP30638 standard; protein; 291 AA.
XX ADP30638;
AC ADP30638;
XX 12-AUG-2004 (first entry)
DT Human secreted protein SEQ ID #1405.
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX Homo sapiens.
XX WO2004035732-A2.
XX 29-APR-2004.
XX 28-AUG-2003; 2003WO-US026780.
XX 29-AUG-2002; 2002US-0406576P.
XX 29-AUG-2002; 2002US-0406579P.
XX 29-AUG-2002; 2002US-0406585P.
XX 29-AUG-2002; 2002US-0406588P.
XX 29-AUG-2002; 2002US-0406608P.
XX 29-AUG-2002; 2002US-0406611P.
XX 29-AUG-2002; 2002US-0406612P.
XX 29-AUG-2002; 2002US-0406616P.
XX 29-AUG-2002; 2002US-0406640P.
XX 29-AUG-2002; 2002US-0406642P.
XX 29-AUG-2002; 2002US-0406646P.
XX 29-AUG-2002; 2002US-0406653P.
XX 29-AUG-2002; 2002US-0406655P.
XX 29-AUG-2002; 2002US-0406666P.
XX 17-SEP-2002; 2002US-0410946P.
XX 17-SEP-2002; 2002US-0410947P.
XX 17-SEP-2002; 2002US-0410948P.
XX 17-SEP-2002; 2002US-0410949P.
XX 17-SEP-2002; 2002US-0410953P.
XX 17-SEP-2002; 2002US-0410957P.
XX 17-SEP-2002; 2002US-0410958P.
XX 17-SEP-2002; 2002US-0410959P.
XX 17-SEP-2002; 2002US-0410960P.
XX 17-SEP-2002; 2002US-0410961P.
XX 17-SEP-2002; 2002US-0410962P.
XX 17-SEP-2002; 2002US-0411019P.
XX 17-SEP-2002; 2002US-0411022P.
XX 17-SEP-2002; 2002US-0411023P.
XX 17-SEP-2002; 2002US-0411024P.
XX 17-SEP-2002; 2002US-0411032P.
XX 17-SEP-2002; 2002US-0411035P.
XX 17-SEP-2002; 2002US-0411037P.
XX 17-SEP-2002; 2002US-0411041P.
XX 17-SEP-2002; 2002US-0411045P.
XX 17-SEP-2002; 2002US-0411046P.
XX 17-SEP-2002; 2002US-0411048P.
XX 17-SEP-2002; 2002US-0411052P.
XX 17-SEP-2002; 2002US-0411055P.
XX 17-SEP-2002; 2002US-0411073P.
XX 17-SEP-2002; 2002US-0411082P.
XX 17-SEP-2002; 2002US-0411101P.
XX 17-SEP-2002; 2002US-0411111P.
XX 18-APR-2003; 2003US-0463700P.
XX 18-APR-2003; 2003US-0463708P.
XX 18-APR-2003; 2003US-0463716P.
XX 02-MAY-2003; 2003US-0467199P.
XX 02-MAY-2003; 2003US-0467201P.
XX 02-MAY-2003; 2003US-0467203P.
XX 19-MAY-2003; 2003US-0467230P.
XX 19-MAY-2003; 2003US-0471306P.
XX 19-MAY-2003; 2003US-0471336P.
XX 22-MAY-2003; 2003US-0472430P.
XX 09-JUN-2003; 2003US-0476609P.
XX 09-JUN-2003; 2003US-0476641P.
XX 08-JUL-2003; 2003US-0485218P.
XX 08-JUL-2003; 2003US-0485223P.

PR 17-SEP-2002; 2002US-0411032P.
 PR 17-SEP-2002; 2002US-0411035P.
 PR 17-SEP-2002; 2002US-0411037P.
 PR 17-SEP-2002; 2002US-0411041P.
 PR 17-SEP-2002; 2002US-0411045P.
 PR 17-SEP-2002; 2002US-0411046P.
 PR 17-SEP-2002; 2002US-0411048P.
 PR 17-SEP-2002; 2002US-0411052P.
 PR 17-SEP-2002; 2002US-0411055P.
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 PR 17-SEP-2002; 2002US-0411082P.
 PR 17-SEP-2002; 2002US-0411101P.
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 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 02-MAY-2003; 2003US-0471306P.
 PR 02-MAY-2003; 2003US-0471336P.
 PR 22-MAY-2003; 2003US-0472420P.
 PR 22-MAY-2003; 2003US-0472430P.
 PR 09-JUN-2003; 2003US-0476609P.
 PR 09-JUN-2003; 2003US-0476641P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 15-JUL-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
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 XX
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 XX
 PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linemann T;
 PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
 XX
 DR WPI; 2004-348438/32.
 XX
 PT New nucleic acid molecule for diagnosing, preventing or treating diseases
 PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
 PT genetic, bacterial and viral diseases.
 XX
 PS Claim 1; SEQ ID NO 2634; 428pp; English.
 XX
 CC The present invention relates to an isolated nucleic acid molecule
 CC encoding a polypeptide which is believed to be cytostatic.
 CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
 CC composition and methods are useful for diagnosing, preventing and
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,
 CC immune, metabolic, genetic, bacterial and viral diseases. The present
 CC sequence represents a human secreted protein. The present sequence is
 CC available on WIPOWEB and is not in the specification.
 XX
 SQ Sequence 291 AA;

Query Match 35.9%; Score 71; DB 8; Length 291;
 Best Local Similarity 57.9%; Pred. No. 9.6;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 13 CGADGACWTWCADGCSRSC 31
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 DB 230 CGAGGCCCTGCAGGCTTC 248

RESULT 10
 ADP30692
 ID ADP30692 standard; protein; 659 AA.
 XX
 AC ADP30692;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human secreted protein SEQ ID #1459.
 XX
 KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
 KW cancer; inflammatory; immune; human secreted protein.
 XX
 OS Homo sapiens.
 PN WO2004035732-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 28-AUG-2003; 2003WO-US026780.
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 PR 29-AUG-2002; 2002US-0406576P.
 PR 29-AUG-2002; 2002US-0406579P.
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 PR 29-AUG-2002; 2002US-0406588P.
 PR 29-AUG-2002; 2002US-0406608P.
 PR 29-AUG-2002; 2002US-0406611P.
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 PR 17-SEP-2002; 2002US-0410946P.
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 PR 17-SEP-2002; 2002US-0411048P.
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 PR 17-SEP-2002; 2002US-0411073P.
 PR 17-SEP-2002; 2002US-0411082P.
 PR 17-SEP-2002; 2002US-0411101P.
 PR 17-SEP-2002; 2002US-0411111P.
 PR 18-APR-2003; 2003US-0463700P.
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 19-MAY-2003; 2003US-0471306P.

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PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RP, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 2690; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOMEB and is not in the specification.
XX
XX SQ Sequence 659 AA;
XX
XX Query Match 35.9%; Score 71; DB 8; Length 659;
XX Best Local Similarity 57.9%; Pred. No. 19;
XX Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
Qy 13 CGADGACWTWCADGCSRC 31
Db ||| ||| ||| ||| :|
35 CGAGGCCCTCGAGGCTTC 53
XX
RESULT 11
ADP30720
ID ADP30720 standard; protein; 659 AA.
XX
AC ADP30720;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human secreted protein SEQ ID #1487.
XX
XX Cytostatic; Antinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
XX Homo sapiens.
XX
XX WO2004035732-A2.
XX
XX 29-APR-2004.
XX
XX 28-AUG-2003; 2003WO-US026780.
XX

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PR 29-AUG-2002; 2002US-0406576P.
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PR 17-SEP-2002; 2002US-0410949P.
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PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
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PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
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PR 19-MAY-2003; 2003US-0471338P.
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PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RP, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI

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Best Local Similarity 57.9%; Pred. No. 19;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 13 CGADGACWTWCADGCSRSC 31
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Db 35 CGAGGCCCTGCAGGCTTTC 53

RESULT 13
ADP30701
ID ADP30701 standard; protein; 659 AA.
AC ADP30701;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human secreted protein SEQ ID #1468.
XX
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
XX Homo sapiens.
XX
XX WO2004035732-A2.
XX
XX 29-APR-2004.
XX
XX 28-AUG-2003; 2003WO-US026780.
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XX 29-AUG-2002; 2002US-0406578P.
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XX 29-AUG-2002; 2002US-0406579P.
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XX 17-SEP-2002; 2002US-0411101P.
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XX 17-SEP-2002; 2002US-0411111P.
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XX 18-APR-2003; 2003US-0463700P.
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XX 18-APR-2003; 2003US-0463708P.
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PR 18-APR-2003; 2003US-0463716P.
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PR 02-MAY-2003; 2003US-0467230P.
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PR 08-JUL-2003; 2003US-0485223P.
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PR 08-JUL-2003; 2003US-0485325P.
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PR 14-JUL-2003; 2003US-0486480P.
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PR 15-JUL-2003; 2003US-0486891P.
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PR 15-JUL-2003; 2003US-0486960P.
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PR 08-AUG-2003; 2003US-0493370P.
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PR 08-AUG-2003; 2003US-0493573P.
PR
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 2699; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPWEB and is not in the specification.
XX
XX Sequence 659 AA;
XX
XX Query Match 35.9%; Score 71; DB 8; Length 659;
XX Best Local Similarity 57.9%; Pred. No. 19;
XX Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 13 CGADGACWTWCADGCSRSC 31
    ||| | | | | | | | | | |
Db 35 CGAGGCCCTGCAGGCTTTC 53

RESULT 14
ADP30712
ID ADP30712 standard; protein; 659 AA.
XX
XX ADP30712;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human secreted protein SEQ ID #1479.
XX
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
XX Homo sapiens.
OS

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XX PN WO2004035732-A2.
XX PD 29-APR-2004.
XX XX
XX PF 28-AUG-2003; 2003WO-US026780.
XX PR 29-AUG-2002; 2002US-0406576P.
XX PR 29-AUG-2002; 2002US-0406579P.
XX PR 29-AUG-2002; 2002US-0406585P.
XX PR 29-AUG-2002; 2002US-0406588P.
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XX PR 29-AUG-2002; 2002US-0406653P.
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XX PR 29-AUG-2002; 2002US-0406666P.
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XX PR 17-SEP-2002; 2002US-0410953P.
XX PR 17-SEP-2002; 2002US-0410957P.
XX PR 17-SEP-2002; 2002US-0410958P.
XX PR 17-SEP-2002; 2002US-0410959P.
XX PR 17-SEP-2002; 2002US-0410960P.
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XX PR 17-SEP-2002; 2002US-0411019P.
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XX PR 17-SEP-2002; 2002US-0411023P.
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XX PR 17-SEP-2002; 2002US-0411055P.
XX PR 17-SEP-2002; 2002US-0411073P.
XX PR 17-SEP-2002; 2002US-0411082P.
XX PR 17-SEP-2002; 2002US-0411101P.
XX PR 17-SEP-2002; 2002US-0411111P.
XX PR 18-APR-2003; 2003US-0463700P.
XX PR 18-APR-2003; 2003US-0463708P.
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XX PR 02-MAY-2003; 2003US-0467199P.
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XX PR 19-MAY-2003; 2003US-0471306P.
XX PR 19-MAY-2003; 2003US-0471336P.
XX PR 22-MAY-2003; 2003US-0472420P.
XX PR 22-MAY-2003; 2003US-0472430P.
XX PR 09-JUN-2003; 2003US-0476609P.
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XX PR 08-JUL-2003; 2003US-0485218P.
XX PR 08-JUL-2003; 2003US-0485223P.
XX PR 08-JUL-2003; 2003US-0485224P.
XX PR 08-JUL-2003; 2003US-0485325P.
XX PR 14-JUL-2003; 2003US-0486446P.
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XX PR 15-JUL-2003; 2003US-0486891P.
XX PR 08-AUG-2003; 2003US-0486960P.
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XX PR 08-AUG-2003; 2003US-0493370P.

PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX XX
XX PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX XX
XX PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX XX
XX DR WPI; 2004-348438/32.
XX XX
XX PT New nucleic acid molecule for diagnosing, preventing or treating diseases
XX PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
XX PT genetic, bacterial and viral diseases.
XX XX
XX PS Claim 1; SEQ ID NO 2710; 428pp; English.
XX XX
XX CC The present invention relates to an isolated nucleic acid molecule
XX CC encoding a polypeptide which is believed to be cytostatic,
XX CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
XX CC composition and methods are useful for diagnosing, preventing and
XX CC treating diseases such as proliferative (e.g. cancer), inflammatory,
XX CC immune, metabolic, genetic, bacterial and viral diseases. The present
XX CC sequence represents a human secreted protein. The present sequence is
XX CC available on WIPOWEB and is not in the specification.
XX XX
XX SQ Sequence 659 AA;

Query Match 35.9%; Score 71; DB 8; Length 659;
Best Local Similarity 57.9%; Pred. No. 19;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 13 CGADGACATWCADGCSRSC 31
Db 35 CGAGCCCTGCAGGCTTTC 53

RESULT 15
ADP30722
ID ADP30722 standard; protein; 659 AA.
XX XX
XX AC ADP30722;
XX XX
XX DT 12-AUG-2004 (first entry)
XX XX
XX DE Human secreted protein SEQ ID #1489.
XX XX
XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
XX KW cancer; inflammatory; immune; human secreted protein.
XX OS Homo sapiens.
XX XX
XX PN WO2004035732-A2.
XX XX
XX PD 29-APR-2004.
XX XX
XX PF 28-AUG-2003; 2003WO-US026780.
XX XX
XX PR 29-AUG-2002; 2002US-0406576P.
XX PR 29-AUG-2002; 2002US-0406579P.
XX PR 29-AUG-2002; 2002US-0406585P.
XX PR 29-AUG-2002; 2002US-0406588P.
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XX PR 29-AUG-2002; 2002US-0406611P.
XX PR 29-AUG-2002; 2002US-0406612P.
XX PR 29-AUG-2002; 2002US-0406616P.
XX PR 29-AUG-2002; 2002US-0406640P.
XX PR 29-AUG-2002; 2002US-0406642P.
XX PR 29-AUG-2002; 2002US-0406646P.
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XX PR 29-AUG-2002; 2002US-0406655P.
XX PR 29-AUG-2002; 2002US-0406666P.
XX PR 17-SEP-2002; 2002US-0410946P.
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PR	17-SEP-2002;	2002US-0411022P
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PR	17-SEP-2002;	2002US-0411037P
PR	17-SEP-2002;	2002US-0411041P
PR	17-SEP-2002;	2002US-0411045P
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PR	17-SEP-2002;	2002US-0411082P
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PR	18-APR-2003;	2003US-0463700P
PR	18-APR-2003;	2003US-0463708P
PR	18-APR-2003;	2003US-0463716P
PR	18-APR-2003;	2003US-0463732P
PR	02-MAY-2003;	2003US-04671199P
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PR	19-MAY-2003;	2003US-0471306P
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PR	22-MAY-2003;	2003US-0472420P
PR	22-MAY-2003;	2003US-0472430P
PR	09-JUN-2003;	2003US-0476609P
PR	09-JUN-2003;	2003US-0476641P
PR	08-JUL-2003;	2003US-0485218P
PR	08-JUL-2003;	2003US-0485223P
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PR	14-JUL-2003;	2003US-0486446P
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PR	15-JUL-2003;	2003US-0486891P
PR	15-JUL-2003;	2003US-0486960P
PR	08-AUG-2003;	2003US-0493341P
PR	08-AUG-2003;	2003US-0493370P
PR	08-AUG-2003;	2003US-0493573P
PR	08-AUG-2003;	2003US-0493577P

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CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPWEB and is not in the specification.
XX
SQ Sequence 659 AA;

Query Match 35.9%; Score 71; DB 8; Length 659;
Best Local Similarity 57.9%; Pred. NO. 19;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps

QY 13 CGADGACWTWCADGCSRSC 31
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Db 35 CGAGGCCCTCGAGGCTTTC 53

Search completed: November 16, 2004, 14:24:18
Job time : 178.642 secs

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XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 2720; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic.
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC

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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:16:01 ; Search time 43.8679 Seconds
(without alignments)
46.865 Million cell updates/sec

Title: US-10-784-537-1

Perfect score: 198
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	67	33.8	61	2	US-08-933-314-25
5	67	33.8	61	4	US-08-472-053-3
6	67	33.8	79	4	US-09-270-767-38435
7	67	33.8	79	4	US-09-270-767-53652
8	64	32.3	61	4	US-08-472-053-2
9	64	32.3	62	4	US-08-472-053-46
10	64	32.3	80	3	US-08-952-383A-14
11	64	32.3	80	3	US-08-970-264A-27
12	64	32.3	85	4	US-09-593-632-22
13	61.5	31.1	5405	3	US-08-718-388-9
14	60.5	30.6	1917	4	US-09-627-650B-5
15	60.5	30.6	1917	4	US-09-436-063C-5
16	60	30.3	2211	3	US-09-738-884-1
17	60	30.3	2211	4	US-10-098-961A-1
18	59.5	30.1	856	4	US-09-699-286A-13
19	59	29.8	61	1	US-08-682-485A-26
20	59	29.8	61	2	US-08-933-314-26
21	59	29.8	61	4	US-08-472-053-4
22	59	29.8	62	1	US-08-451-472-5
23	59	29.8	83	4	US-09-252-991A-18845
24	59	29.8	85	4	US-09-599-632-23
25	59	29.8	2732	4	US-09-086-436-30
26	58.5	29.5	63	4	US-09-252-991A-22358
27	58.5	29.5	2088	4	US-09-548-372D-13

28	58.5	29.5	2088	4	US-09-548-367D-13	Sequence 13, Appl
29	58.5	29.5	2088	4	US-09-551-853D-13	Sequence 13, Appl
30	58.5	29.5	2088	4	US-09-548-376D-13	Sequence 13, Appl
31	58.5	29.5	2088	4	US-09-548-373D-13	Sequence 13, Appl
32	58.5	29.5	2088	4	US-09-548-366F-13	Sequence 13, Appl
33	58	29.3	339	4	US-09-252-991A-19249	Sequence 19249, A
34	58	29.3	339	4	US-09-627-650B-7	Sequence 7, Appl
35	58	29.3	2508	4	US-09-436-063C-7	Sequence 7, Appl
36	58	29.3	2544	4	US-09-627-650B-3	Sequence 3, Appl
37	58	29.3	2544	4	US-09-436-063C-3	Sequence 3, Appl
38	58	29.3	2601	4	US-09-627-650B-9	Sequence 9, Appl
39	58	29.3	2601	4	US-09-436-063C-9	Sequence 9, Appl
40	57.5	29.0	156	4	US-09-270-767-33322	Sequence 33322, A
41	57.5	29.0	156	4	US-09-270-767-48539	Sequence 48539, A
42	57.5	29.0	206	3	US-08-820-970-9	Sequence 9, Appl
43	57.5	29.0	2813	3	US-08-896-449A-2	Sequence 2, Appl
44	57.5	29.0	2813	3	US-09-132-652-2	Sequence 2, Appl
45	57.5	29.0	2813	4	US-09-886-900A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-451-472-6
; Sequence 6, Application US/08451472
; Patent No. 5770192
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 5770192th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,125
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-187
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816 4000
; TELEFAX: (703) 816 4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-472-6

Query Match 33.8%; Score 67; DB 1; Length 60;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 NLCIRECESICGADGACWTW 22
| | | | |
Db 18 NECDECKAYGGSGYCVTW 37

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1  TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
2  NUMBER OF SEQUENCES: 73
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Nixon & Vanderhye PC
5  STREET: 8th Floor, 1100 No. 5770192th Glebe Road
6  CITY: Arlington
7  STATE: Virginia
8  COUNTRY: USA
9  ZIP: 22201-4714
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patentin Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/451,472
17 FILING DATE:
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/117,125
21 FILING DATE: 24-NOV-1993
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Mary J Wilson
24 REGISTRATION NUMBER: 32,955
25 REFERENCE/DOCKET NUMBER: 117-187
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (703) 816 4000
28 TELEFAX: (703) 816 4100
29 TELEX: 200797 NIXN UR
30 INFORMATION FOR SEQ ID NO: 4:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 61 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: peptide
36 US-08-451-472-4
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38 Query Match 33.8%; Score 67; DB 1; Length 61;
39 Best Local Similarity 55.6%; Pred. No. 1.9;
40 Matches 10; Conservative 3; Mismatches 5; Indels 0
41
42 QY 5 CIRECESICGADGACWTW 22
43 | : | | | : | | | |
44 DB 21 CNKECKSYGGSYGYCWTW 38
45
46 RESULT 4
47 US-08-933-314-25
48 Sequence 25, Application US/08933314
49 Patent No. 5959182
50 GENERAL INFORMATION:
51 APPLICANT: ATKINSON, RONALD K
52 APPLICANT: HOWDEN, MERLIN E.H.
53 APPLICANT: TYLER, MARGARET I
54 APPLICANT: VONARX, EDWARD J
55 TITLE OF INVENTION: Insecticidal Toxins Derived From
56 TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
57 NUMBER OF SEQUENCES: 26
58 CORRESPONDENCE ADDRESS:
59 ADDRESSEE: Zeneca, Inc.
60 STREET: 1200 South 47th Street
61 CITY: Richmond
62 STATE: California
63 COUNTRY: USA
64 ZIP: 94804
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 COMPUTER: IBM PC compatible
68 OPERATING SYSTEM: PC-DOS/MS-DOS
69 SOFTWARE: Patentin Release #1.0, Version #1.25
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER: US/08/933,314
72 FILING DATE:

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; Sequence 14, Application US/08952383A
; Patent No. 6096304
; GENERAL INFORMATION:
; APPLICANT:

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1 CLASSIFICATION:
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3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 60/009,120
5 FILING DATE: DECEMBER 22, 1995
6 ATTORNEY/AGENT INFORMATION:
7
8 NAME: BEARDELL, LORI Y.
9 REGISTRATION NUMBER: 34,293
10 REFERENCE/DOCKET NUMBER: BA-9078
11
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 302-992-4926
14 TELEFAX: 302-773-0164
15 INFORMATION FOR SEQ ID NO: 27:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 80 amino acids
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19 STRANDEDNESS: single
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US-08-970-264A-27

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DB 40 CDKECKAYGSGYGCWTW 57

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; Sequence 22, Application US/09599632
; Patent No. 6768002
; GENERAL INFORMATION:
; APPLICANT: Herriman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1375 US NA
; CURRENT APPLICATION NUMBER: US/09/599,632
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,410
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Leiurus quinquestriatus
US-09-599-632-22

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Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTW 22
DB 42 CDKECKAYGSGYGCWTW 59

RESULT 13
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IgG Fc REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-388-9

Query Match      31.1%; Score 61.5; DB 3; Length 5405;
Best Local Similarity 41.4%; Pred. No. 3.5e+02;
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RESULT 14
US-09-627-650B-5
; Sequence 5, Application US/09627650B
; Patent No. 6406872
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 21101.0009U3
; CURRENT APPLICATION NUMBER: US/09/627,650B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/436,063
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107,727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-627-650B-5

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QY 5 CIRECESICGADGACWTWCADGCSRSC 31
DB 944 CAGTCTATCAAGGTGCT-CAATCATAC 969

RESULT 15
US-09-436-063C-5
; Sequence 5, Application US/09436063C
; Patent No. 6407210
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: P-1095corrected
; CURRENT APPLICATION NUMBER: US/09/436,063C
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 18
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
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US-09-436-063C-5

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Db 944 CAGTCTATCAAGGTGCT-CAATCATAC 969

Search completed: November 16, 2004, 14:32:10
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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75.615 Million cell updates/sec

Title: US-10-784-537-1

Perfect score: 198

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	71	35.9	3147	15 US-10-307-817-563	Sequence 563, App
4	71	35.9	3288	14 US-10-184-644-477	Sequence 477, App
5	71	35.9	3288	14 US-10-184-634-477	Sequence 477, App
6	70.5	35.6	7285	14 US-10-145-206-28	Sequence 28, App1
7	70	35.4	3233	14 US-10-123-155-81	Sequence 81, App1
8	70	35.4	3233	14 US-10-146-731-81	Sequence 81, App1
9	70	35.4	3233	14 US-10-140-472-81	Sequence 81, App1
10	70	35.4	3233	14 US-10-141-761-81	Sequence 81, App1
11	70	35.4	3233	14 US-10-142-885-81	Sequence 81, App1
12	70	35.4	3233	14 US-10-158-790-81	Sequence 81, App1
13	70	35.4	3233	14 US-10-137-871-81	Sequence 81, App1

14	70	35.4	3233	14	US-10-140-923-81	Sequence 81, App1
15	70	35.4	3233	14	US-10-141-756-81	Sequence 81, App1
16	70	35.4	3233	14	US-10-141-759-81	Sequence 81, App1
17	70	35.4	3233	14	US-10-140-805-81	Sequence 81, App1
18	70	35.4	3233	14	US-10-140-864-81	Sequence 81, App1
19	70	35.4	3233	15	US-10-142-426-81	Sequence 81, App1
20	69.5	35.1	1401	10	US-09-759-130B-177	Sequence 177, App
21	69.5	35.1	1401	16	US-10-741-790-177	Sequence 177, App
22	69	34.8	1475	14	US-10-123-155-491	Sequence 491, App
23	69	34.8	1475	14	US-10-146-731-491	Sequence 491, App
24	69	34.8	1475	14	US-10-140-472-491	Sequence 491, App
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27	69	34.8	1475	14	US-10-158-790-491	Sequence 491, App
28	69	34.8	1475	14	US-10-063-685-79	Sequence 79, App1
29	69	34.8	1475	14	US-10-137-871-491	Sequence 491, App
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31	69	34.8	1475	14	US-10-141-756-491	Sequence 491, App
32	69	34.8	1475	14	US-10-141-759-491	Sequence 491, App
33	69	34.8	1475	14	US-10-140-805-491	Sequence 491, App
34	69	34.8	1475	14	US-10-140-864-491	Sequence 491, App
35	69	34.8	1475	15	US-10-142-426-491	Sequence 491, App
36	68	34.3	2476	14	US-10-184-644-585	Sequence 585, App
37	68	34.3	2476	14	US-10-184-634-585	Sequence 585, App
38	68	34.3	4333	14	US-10-123-155-233	Sequence 233, App
39	68	34.3	4333	14	US-10-146-731-233	Sequence 233, App
40	68	34.3	4333	14	US-10-140-472-233	Sequence 233, App
41	68	34.3	4333	14	US-10-141-761-233	Sequence 233, App
42	68	34.3	4333	14	US-10-142-885-233	Sequence 233, App
43	68	34.3	4333	14	US-10-158-790-233	Sequence 233, App
44	68	34.3	4333	14	US-10-137-871-233	Sequence 233, App
45	68	34.3	4333	14	US-10-140-923-233	Sequence 233, App

ALIGNMENTS

RESULT 1

US-10-363-204-125
; Sequence 125, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774_P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(31)
; OTHER INFORMATION: synthetic construct
US-10-363-204-125

Query Match Best Local Similarity 100.0%; Score 198; DB 16; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31

Db 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31

RESULT 2

US-10-307-817-562
; Sequence 562, Application US/10307817
; Publication No. US2004005838A1
; GENERAL INFORMATION:

; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 562
; LENGTH: 3147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-562

Query Match 35.9%; Score 71; DB 15; Length 3147;
Best Local Similarity 41.9%; Pred. No. 36;
Matches 13; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31
Db 916 CGGCCATCC--CCGAGGGCCTCCCGGTGTC 944

RESULT 3
US-10-307-817-563
; Sequence 563, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 563
; LENGTH: 3147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-563

Query Match 35.9%; Score 71; DB 15; Length 3147;
Best Local Similarity 41.9%; Pred. No. 36;
Matches 13; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31
Db 916 CGGCCATCC--CCGAGGGCCTCCCGGTGTC 944

RESULT 4
US-10-184-644-477
; Sequence 477, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 477

; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-477

Query Match 35.9%; Score 71; DB 14; Length 3288;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 13 CGADGACWTWCADGCSRSC 31
Db 1741 CGAGGCCCTGCAGGCTTTC 1759

RESULT 5
US-10-184-634-477
; Sequence 477, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 477
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-477

Query Match 35.9%; Score 71; DB 14; Length 3288;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 13 CGADGACWTWCADGCSRSC 31
Db 1741 CGAGGCCCTGCAGGCTTTC 1759

RESULT 6
US-10-145-206-28
; Sequence 28, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 7285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:


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; OTHER INFORMATION: pAMG21-RANK-Pc vector
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Xaa (Pos1,2,3,15,16,17) are each independently absent or amino acid residues;
; OTHER INFORMATION: id residues;
; OTHER INFORMATION: Xaa (Pos5,6,7,9,13) are each independently amino acid residues.
US-10-145-206-28

Query Match      35.6%; Score 70.5; DB 14; Length 7285;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 14; Conservative 1; Mismatches 13; Indels 7; Gaps 1;

Qy 1 CYNLCIRCESICGADGACWTWC-----ADGCS 28
Db 4338 CCGTCTTACTGCGAAGACGTCGTAAACGTATGCA 4372

RESULT 7
US-10-123-155-81
; Sequence 81, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123.155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-81

Query Match      35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRCESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770

RESULT 8
US-10-146-731-81
; Sequence 81, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: US/10/140.472
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-472-81

Query Match      35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRCESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770

RESULT 9
US-10-140-472-81
; Sequence 81, Application US/10140472
; Publication No. US20030138888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: US/10/140.472
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-472-81

Query Match      35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRCESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770
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Db 744 CCTACCTTCAGGACCTCTGGCCTGC 770

RESULT 10

US-10-141-761-81
; Sequence 81, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198

; CURRENT APPLICATION NUMBER: US/10/141,761
; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 81

; LENGTH: 3233

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-141-761-81

Query Match 35.4%; Score 70; DB 14; Length 3233;

Best Local Similarity 44.4%; Pred. No. 47;

Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTWCADGCSRSC 31

Db 744 CCTACCTTCAGGACCTCTGGCCTGC 770

RESULT 11

US-10-142-885-81

; Sequence 81, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248

; CURRENT APPLICATION NUMBER: US/10/142,885

; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 81

; LENGTH: 3233

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-142-885-81

Query Match 35.4%; Score 70; DB 14; Length 3233;

Best Local Similarity 44.4%; Pred. No. 47;

Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTWCADGCSRSC 31

Db 744 CCTACCTTCAGGACCTCTGGCCTGC 770

RESULT 12

US-10-158-790-81

; Sequence 81, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C448

; CURRENT APPLICATION NUMBER: US/10/158,790

; CURRENT FILING DATE: 2002-05-30

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 81

; LENGTH: 3233

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-158-790-81

Query Match 35.4%; Score 70; DB 14; Length 3233;

Best Local Similarity 44.4%; Pred. No. 47;

Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 5 CIRECESICGADGACWTWCADGCSRSC 31

Db 744 CCTACCTTCAGGACCTCTGGCCTGC 770

RESULT 13

US-10-137-871-81

; Sequence 81, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

```
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC153
; CURRENT APPLICATION NUMBER: US/10/137,871
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-871-81

Query Match 35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRECESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770

RESULT 14
US-10-140-923-81
; Sequence 81, Application US/10140923
; Publication No. US20030207355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC188
; CURRENT APPLICATION NUMBER: US/10/140,923
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-923-81

Query Match 35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRECESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770

RESULT 14
US-10-140-923-81
; Sequence 81, Application US/10140923
; Publication No. US20030207355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC188
; CURRENT APPLICATION NUMBER: US/10/140,923
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-923-81

Query Match 35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRECESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770
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Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770

RESULT 15
US-10-141-756-81
; Sequence 81, Application US/10141756
; Publication No. US20030207359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC200
; CURRENT APPLICATION NUMBER: US/10/141,756
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-756-81

Query Match 35.4%; Score 70; DB 14; Length 3233;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 12; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CIRECESICGADGACWTWCADGCSRSC 31
Db 744 CCTACCTTCAGGACCTCTGCGCTGC 770

Search completed: November 16, 2004, 14:51:27
Job time : 146.057 secs
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:19:17 ; Search time 505.943 Seconds
(without alignments)
67.889 Million cell updates/sec

Title: US-10-784-537-1

Perfect score: 198

Sequence: 1 CYNLCIRECSICGADGACWTWCADGCSRSC 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	198	100.0	31	1	PCT-US01-27692A-125	Sequence 125, App
2	198	100.0	31	1	PCT-US02-27836-58	Sequence 58, Appl
3	198	100.0	31	29	US-10-363-204-125	Sequence 125, App
4	198	100.0	31	33	US-10-784-537-1	Sequence 1, Appli
5	198	100.0	31	33	US-10-784-537-9	Sequence 9, Appli
6	73	36.9	2808	1	PCT-US03-26780-3256	Sequence 3256, Ap
7	73	36.9	4683	1	PCT-US03-26780-3258	Sequence 3258, Ap
8	73	36.9	4848	1	PCT-US03-26780-3257	Sequence 3257, Ap
9	71.5	36.1	2027	1	PCT-US03-26780-3056	Sequence 3056, Ap
10	71	35.9	291	1	PCT-US03-26780-2634	Sequence 2634, Ap
11	71	35.9	291	1	PCT-US03-26780-2636	Sequence 2636, Ap
12	71	35.9	291	1	PCT-US03-26780-2637	Sequence 2637, Ap
13	71	35.9	659	1	PCT-US03-26780-2690	Sequence 2690, Ap
14	71	35.9	659	1	PCT-US03-26780-2697	Sequence 2697, Ap
15	71	35.9	659	1	PCT-US03-26780-2699	Sequence 2699, Ap
16	71	35.9	659	1	PCT-US03-26780-2710	Sequence 2710, Ap
17	71	35.9	659	1	PCT-US03-26780-2718	Sequence 2718, Ap
18	71	35.9	659	1	PCT-US03-26780-2720	Sequence 2720, Ap
19	71	35.9	1478	1	PCT-US03-26780-2563	Sequence 2563, Ap
20	71	35.9	2803	1	PCT-US03-26780-2747	Sequence 2747, Ap
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22	71	35.9	3147	29	US-10-307-817-563	Sequence 563, App
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24	71	35.9	3288	27	US-10-176-912-477	Sequence 477, App
25	71	35.9	3288	27	US-10-179-524-477	Sequence 477, App
26	71	35.9	3288	27	US-10-184-634-477	Sequence 477, App
27	71	35.9	3288	27	US-10-184-644-477	Sequence 477, App
28	71	35.9	4706	36	US-60-592-191-185	Sequence 185, App
29	71	35.9	4725	36	US-60-592-191-190	Sequence 190, App
30	71	35.9	4812	36	US-60-592-191-189	Sequence 189, App
31	70.5	35.6	7285	1	PCT-US02-15273-28	Sequence 28, Appl
32	70.5	35.6	7285	27	US-10-145-206-28	Sequence 28, Appl
33	70.5	35.6	7285	27	US-10-145-206A-28	Sequence 28, Appl
34	70	35.4	291	1	PCT-US03-26780-2628	Sequence 2628, Ap
35	70	35.4	291	1	PCT-US03-26780-2631	Sequence 2631, Ap
36	70	35.4	375	1	PCT-US03-26780-2604	Sequence 2604, Ap
37	70	35.4	3233	27	US-10-137-871-81	Sequence 81, Appl
38	70	35.4	3233	27	US-10-158-790-81	Sequence 81, Appl
39	70	35.4	3399	1	PCT-US04-07434-47	Sequence 47, Appl
40	69.5	35.1	60	3	US-07-629-603-7	Sequence 7, Appli
41	69.5	35.1	1401	22	US-09-759-1308-177	Sequence 177, App
42	69.5	35.1	1401	33	US-10-741-790-177	Sequence 177, App
43	69.5	35.1	2700	1	PCT-US03-26780-2908	Sequence 2908, Ap
44	69.5	35.1	2700	1	PCT-US03-26780-2909	Sequence 2909, Ap
45	69	34.8	1475	26	US-10-063-545-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
PCT-US01-27692A-125
; Sequence 125, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(31)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-125

Query Match	100.0%;	Score 198;	DB 29;	Length 31;
Best Local Similarity	100.0%;	Pred. No. 4.3e-14;		
Matches 31;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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RESULT 5
US-10-784-537-9
; Sequence 9, Application US/10784537
; GENERAL INFORMATION:
; APPLICANT: ARAP, WADIH
; APPLICANT: PASQUALINI
; APPLICANT: MARCHIO, SERENA
; APPLICANT: LAHDENRANTA, JOHANNA
; TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
; TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
; FILE REFERENCE: UTSC:872US
; CURRENT APPLICATION NUMBER: US/10/784,537
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/27692
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/765,101
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/231,266
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1

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; SEQ ID NO 9
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-784-537-9

Query Match      100.0%; Score 198; DB 33; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.3e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
Db 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31

RESULT 6
PCT-US03-26780-3256
; Sequence 3256, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3256
; LENGTH: 2808
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-3256

Query Match      36.9%; Score 73; DB 1; Length 2808;
Best Local Similarity 45.2%; Pred. No. 67;
Matches 14; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
Db 1974 CTTTCTGTCCACGAGGACCTGC--GCTTCC 2002

RESULT 7
PCT-US03-26780-3258
; Sequence 3258, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3258
; LENGTH: 2808
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-3258

Query Match      36.9%; Score 73; DB 1; Length 2808;
Best Local Similarity 45.2%; Pred. No. 67;
Matches 14; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
Db 1974 CTTTCTGTCCACGAGGACCTGC--GCTTCC 2002

RESULT 8
PCT-US03-26780-3257
; Sequence 3257, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3257
; LENGTH: 2808
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-3257

Query Match      36.9%; Score 73; DB 1; Length 4683;
Best Local Similarity 45.2%; Pred. No. 1e+02;
Matches 14; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
Db 2049 CTTTCTGTCCACGAGGACCTGC--GCTTCC 2077
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; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3257

; LENGTH: 4848

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-26780-3257

Query Match 36.9%; Score 71; DB 1; Length 4848;

Best Local Similarity 45.2%; Pred. No. 1e+02;

Matches 14; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31

Db 2214 CTTTCTGTCCACGAGGACCTGC--GCTTCC 2242

RESULT 9

PCT-US03-26780-3056

; Sequence 3056, Application PC/TUS0326780

; GENERAL INFORMATION:

; APPLICANT: FIVEPRIME THERAPEUTICS, INC.

; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF

; TITLE OF INVENTION: THEIR USE

; FILE REFERENCE: 08940.0014-00304

; CURRENT APPLICATION NUMBER: PCT/US03/26780

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: 60/406,616

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,579

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,655

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,642

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,640

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,588

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,576

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,646

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,666

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,653

; PRIOR FILING DATE: 2002-08-29

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3700

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3056

; LENGTH: 2027

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-26780-3056

Query Match 36.1%; Score 71.5; DB 1; Length 2027;

Best Local Similarity 45.2%; Pred. No. 76;

Matches 14; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

QY 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31

Db 887 CAACCTGTCTCCGAGGACCTACCGGCCCTC 916

RESULT 10

PCT-US03-26780-2634

; Sequence 2634, Application PC/TUS0326780

; GENERAL INFORMATION:

; APPLICANT: FIVEPRIME THERAPEUTICS, INC.

; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF

; TITLE OF INVENTION: THEIR USE

; FILE REFERENCE: 08940.0014-00304

; CURRENT APPLICATION NUMBER: PCT/US03/26780

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: 60/406,616

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,579

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,655

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,642

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,640

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,588

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,576

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,646

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,666

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,653

; PRIOR FILING DATE: 2002-08-29

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3700

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2634

; LENGTH: 291

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-26780-2634

Query Match 35.9%; Score 71; DB 1; Length 291;

Best Local Similarity 57.9%; Pred. No. 19;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 13 CGADGACWTWCADGCSRSC 31

Db 230 CGAGGCCCTGCAGGCTTTC 248

RESULT 11

PCT-US03-26780-2636

; Sequence 2636, Application PC/TUS0326780

; GENERAL INFORMATION:

; APPLICANT: FIVEPRIME THERAPEUTICS, INC.

; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF

; TITLE OF INVENTION: THEIR USE

; FILE REFERENCE: 08940.0014-00304

; CURRENT APPLICATION NUMBER: PCT/US03/26780

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: 60/406,616

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,579

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,655

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,642

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,640

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,588

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,576

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,646

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,666

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 60/406,653

; PRIOR FILING DATE: 2002-08-29

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3700

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2636

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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
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; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2690
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US03-26780-2690

Query Match          35.9%; Score 71; DB 1; Length 659;
Best Local Similarity 57.9%; Pred. No. 16;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      13  CGAGGACWTWCADGCSRSC 31
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Db       35  CGAGGCCCTGCAGGCTTTC 53

RESULT 14
PCT-US03-26780-2697
; Sequence 2697, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
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; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2697
; LENGTH: 659
; TYPE: PRT

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; ORGANISM: Homo sapiens
PCT-US03-26780-2697

Query Match      35.9%; Score 71; DB 1; Length 659;
Best Local Similarity 57.9%; Pred. No. 36;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 13 CGADGACWTWCADGCSRSC 31
   ||| ||| ||| ||| :|
Db 35 CGAGGCCCTGCAGGCTTTC 53

RESULT 15
PCT-US03-26780-2699
; Sequence 2699, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2699
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-2699

Query Match      35.9%; Score 71; DB 1; Length 659;
Best Local Similarity 57.9%; Pred. No. 36;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 13 CGADGACWTWCADGCSRSC 31
   ||| ||| ||| ||| :|
Db 35 CGAGGCCCTGCAGGCTTTC 53

Search completed: November 16, 2004, 14:46:42
Job time : 506.943 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:24:42 ; Search time 5.88679 Seconds
(without alignments)
40.083 Million cell updates/sec

Title: US-10-784-537-3

Perfect score: 84

Sequence: 1 CPKVCPRCESNC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 80665 seqs, 18150633 residues

Total number of hits satisfying chosen parameters: 80665

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/prodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	13	6	US-10-489-071-60
2	53	63.1	844	6	US-10-411-910B-48
3	50	59.5	9	6	US-10-489-071-56
4	47	56.0	31	6	US-10-489-071-58
5	47	56.0	383	5	US-09-963-693B-105
6	46	54.8	80	6	US-10-976-102-52
7	46	54.8	2471	6	US-10-765-727-23
8	46	54.8	2471	6	US-10-846-989-57
9	45	53.6	110	6	US-10-883-805-3
10	45	53.6	1363	6	US-10-732-923-13625
11	44	52.4	80	6	US-10-976-102-89
12	44	52.4	370	5	US-09-963-693B-104
13	44	52.4	1370	6	US-10-482-029-229
14	44	52.4	1382	8	US-60-616-596-20
15	44	52.4	2768	6	US-10-510-101-72
16	43	51.2	388	6	US-10-220-366A-16731
17	43	51.2	599	6	US-10-734-049A-215
18	43	51.2	627	6	US-10-220-366A-27561
19	42	50.0	110	6	US-10-883-805-13
20	42	50.0	244	6	US-10-732-923-5365
21	42	50.0	564	6	US-10-732-923-9253
22	42	50.0	598	6	US-10-732-923-14189
23	42	50.0	695	6	US-10-732-923-14197
24	42	50.0	842	6	US-10-732-923-14188
25	42	50.0	1077	6	US-10-732-923-14210

26	41.5	49.4	500	5	US-09-978-191B-363	Sequence 363, App
27	41.5	49.4	500	5	US-09-999-829B-363	Sequence 363, App
28	41.5	49.4	733	6	US-10-732-923-14218	Sequence 14218, A
29	41	48.8	96	6	US-10-976-102-65	Sequence 65, Appl
30	41	48.8	146	6	US-10-220-366A-14308	Sequence 14308, A
31	41	48.8	182	6	US-10-732-923-5576	Sequence 5576, Ap
32	41	48.8	225	6	US-10-732-923-5350	Sequence 5350, Ap
33	41	48.8	253	6	US-10-732-923-5545	Sequence 5545, Ap
34	40	47.6	116	6	US-10-399-103A-842	Sequence 842, App
35	40	47.6	495	6	US-10-732-923-1204	Sequence 1204, Ap
36	40	47.6	1297	6	US-10-821-630A-1	Sequence 1, Appli
37	39.5	47.0	245	6	US-10-732-923-14190	Sequence 14190, A
38	39.5	47.0	994	6	US-10-732-923-14191	Sequence 14191, A
39	39	46.4	80	6	US-10-976-102-78	Sequence 78, Appl
40	39	46.4	80	6	US-10-976-102-79	Sequence 79, Appl
41	39	46.4	80	6	US-10-976-102-96	Sequence 96, Appl
42	39	46.4	110	6	US-10-399-103A-833	Sequence 833, App
43	39	46.4	118	6	US-10-883-805-2	Sequence 2, Appli
44	39	46.4	211	6	US-10-980-388-97	Sequence 97, Appl
45	39	46.4	225	6	US-10-732-923-5731	Sequence 5731, Ap

ALIGNMENTS

RESULT 1
US-10-489-071-60
; Sequence 60, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUALINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-60

Query Match 100.0%; Score 84; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPKVCPRCESNC 13
| | | | | | | | | | | | | |
Db 1 CPKVCPRCESNC 13

RESULT 2
US-10-411-910B-48
; Sequence 48, Application US/10411910B
; GENERAL INFORMATION:
; APPLICANT: DILLON, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910B
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Desulfitobacterium hafniense
US-10-411-910B-48

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Query Match      63.1%; Score 53; DB 6; Length 844;
Best Local Similarity 53.8%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 13
Db      177 CORVCPHSCQAQC 189

RESULT 3
US-10-489-071-56
; Sequence 56, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUALINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-56

Query Match      59.5%; Score 50; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.4e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CPRECESNC 13
Db      1 CPRECESIC 9

RESULT 4
US-10-489-071-58
; Sequence 58, Application US/10489071
; GENERAL INFORMATION:
; APPLICANT: PASQUALINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
; FILE REFERENCE: UTSC:856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-58

Query Match      56.0%; Score 47; DB 6; Length 31;
Best Local Similarity 61.5%; Pred. No. 0.71;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 13
Db      1 CYNLCIRECESIC 13

RESULT 5
US-09-963-693B-105
```

```
; Sequence 105, Application US/09963693B
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693B
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-963-693B-105

Query Match      56.0%; Score 47; DB 5; Length 383;
Best Local Similarity 46.2%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 13
Db      86 CQTKCPEKCRNNC 98

RESULT 6
US-10-976-102-52
; Sequence 52, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 05/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-976-102-52

Query Match      54.8%; Score 46; DB 6; Length 80;
Best Local Similarity 58.3%; Pred. No. 2.4;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 12
Db      43 CPKVCAGRCANN 54

RESULT 7
US-10-765-727-23
; Sequence 23, Application US/10765727
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
```

; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
; FILE REFERENCE: 674525-2010
; CURRENT APPLICATION NUMBER: US/10/765,727
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03426
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: GB 0118153.6
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: GB 0207930.9
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB 0212282.8
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: GB 0212283.6
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-765-727-23

Query Match 54.8%; Score 46; DB 6; Length 2471;
Best Local Similarity 61.5%; Pred. No. 58;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRCESNC 13
|||:|||||
Db 1368 CPS--PRDCSGC 1378

RESULT 8
US-10-846-989-57
; Sequence 57, Application US/10846989
; GENERAL INFORMATION:
; APPLICANT: BOOMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: RAGNO, SILVIA
; APPLICANT: TUGAL, TAMARA
; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MEDICAL TREATMENT
; FILE REFERENCE: 654525-2012
; CURRENT APPLICATION NUMBER: US/10/846,989
; CURRENT FILING DATE: 2004-05-14
; PRIOR FILING DATE: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0127271.5
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 57
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-846-989-57

Query Match 54.8%; Score 46; DB 6; Length 2471;
Best Local Similarity 61.5%; Pred. No. 58;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRCESNC 13
|||:|||||
Db 1368 CPS--PRDCSGC 1378

RESULT 9
US-10-883-805-3

; Sequence 3, Application US/10883805
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; TITLE OF INVENTION: HUMAN EPIDERMAL PROTEINS
; FILE REFERENCE: PF-0567 PCT
; CURRENT APPLICATION NUMBER: US/10/883,805
; CURRENT FILING DATE: 2004-07-06
; PRIOR FILING DATE: 09/123,531
; PRIOR APPLICATION NUMBER: unassigned
; PRIOR FILING DATE: 1998-07-28
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 09/206,817
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: unassigned
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 1798487
US-10-883-805-3

Query Match 53.6%; Score 45; DB 6; Length 110;
Best Local Similarity 46.2%; Pred. No. 4.3;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
|||:|||||
Db 28 CPPKCPQCPAPC 40

RESULT 10
US-10-732-923-13625
; Sequence 13625, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Egerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13625
; LENGTH: 1363
; TYPE: PRT
; ORGANISM: Cynops pyrrhogaster
US-10-732-923-13625

Query Match 53.6%; Score 45; DB 6; Length 1363;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPKVCPRC 9
|||:|||||
Db 213 CQKVCPRC 221

RESULT 11
US-10-976-102-89
; Sequence 89, Application US/10976102
; GENERAL INFORMATION:

```
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-10-976-102-89

Query Match          52.4%; Score 44; DB 6; Length 80;
Best Local Similarity 50.0%; Pred. No. 4.4;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 PKVCPRECSNC 13
DB      42 PEECPACEYRC 53

RESULT 12
US-09-963-693B-104
; Sequence 104, Application US/09963693B
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693B
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-963-693B-104

Query Match          52.4%; Score 44; DB 5; Length 370;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPKVCPCRECSN 12
DB      75 CQKVCPTICKSH 86

RESULT 13
US-10-482-029-229
; Sequence 229, Application US/10482029
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29

; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: US/10/976,102
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-10-976-102-89

Query Match          52.4%; Score 44; DB 6; Length 1370;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPKVCPCRECSN 12
DB      215 CQKVCPTICKSH 226

RESULT 14
US-60-616-596-20
; Sequence 20, Application US/60616596
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail
; APPLICANT: Roberts, Charles T
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING DISEASE
; FILE REFERENCE: 49321-125
; CURRENT APPLICATION NUMBER: US/60/616,596
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1382
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-60-616-596-20

Query Match          52.4%; Score 44; DB 8; Length 1382;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CPKVCPCRECSN 12
DB      215 CQKVCPTICKSH 226

RESULT 15
US-10-510-101-72
; Sequence 72, Application US/10510101
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 2768
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (734)..(734)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1028)..(1028)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2501)..(2501)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-510-101-72
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Query Match          52.4%; Score 44; DB 6; Length 2768;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PKVCPRECE 10
Db      157 PKRCPRSC 165
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Search completed: November 16, 2004, 14:47:13
Job time : 6.88679 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:15:03 ; Search time 14.717 Seconds
(without alignments)
84.991 Million cell updates/sec

Title: US-10-784-537-3

Perfect score: 84

Sequence: 1 CPKVCPECSNC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	64.3	1363	2 T43220	insulin-like growt
2	53	63.1	425	2 AE2094	hypothetical prote
3	52	61.9	413	2 JE0142	glutamate synthase
4	51	60.7	468	2 H72230	glutamate synthase
5	50	59.5	51	1 XKPOT	proteinase inhibit
6	50	59.5	105	2 G95318	FdxB ferredoxin II
7	50	59.5	1321	2 JE0352	mucin MUC5B, trach
8	50	59.5	1513	2 T23681	hypothetical prote
9	49	58.3	476	2 A70477	glutamate synthase
10	49	58.3	481	2 A46602	glutamate synthase
11	49	58.3	481	2 D87696	glutamate synthase
12	48	57.1	142	2 B41132	collagen-related p
13	47	56.0	102	1 FERF3C	ferredoxin 2(4Fe-4
14	47	56.0	412	2 H85852	probable oxidoredu
15	47	56.0	412	2 A64983	hypothetical prote
16	47	56.0	412	2 F91008	probable oxidoredu
17	47	56.0	2101	2 S57245	insulin receptor (
18	47	56.0	2148	1 A56081	insulin receptor -
19	46	54.8	204	2 T08072	proteinase inhibit
20	46	54.8	320	2 T09288	late embryonic abu
21	46	54.8	388	2 T31887	hypothetical prote
22	46	54.8	388	2 T31888	hypothetical prote
23	46	54.8	395	2 S75952	hypothetical prote
24	46	54.8	438	2 T31889	hypothetical prote
25	46	54.8	445	2 T31898	hypothetical prote
26	46	54.8	573	2 JC4335	anti-mullerian hor
27	45	53.6	342	2 T16735	hypothetical prote
28	45	53.6	471	2 G82083	glutamate synthase
29	45	53.6	472	2 G85985	glutamate synthase

30	45	53.6	472	2 AB0907	glutamate synthase
31	45	53.6	472	2 D91140	glutamate synthase
32	45	53.6	472	2 G65112	glutamate synthase
33	45	53.6	472	2 AG0432	glutamate synthase
34	45	53.6	487	2 B89813	NADH-glutamate syn
35	45	53.6	494	2 H82523	glutamate synthase
36	45	53.6	671	2 AF0042	probable oxidoredu
37	45	53.6	728	2 T20561	hypothetical prote
38	44.5	53.0	158	2 T07597	proteinase inhibit
39	44	52.4	52	1 TIE01	proteinase inhibit
40	44	52.4	53	2 JQ2269	trypsin inhibitor-
41	44	52.4	103	2 A84713	probable gibberell
42	44	52.4	147	2 S24973	proteinase inhibit
43	44	52.4	154	2 S43105	proteinase inhibit
44	44	52.4	397	2 JQ2153	proteinase inhibit
45	44	52.4	479	2 E86785	glutamate synthase

ALIGNMENTS

RESULT 1

T43220
insulin-like growth factor-1 receptor - common lancelet
N;Alternate names: insulin-like peptide receptor
C;Species: Branchiostoma lanceolatum (common lancelet)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43220
R;Pashmforoush, M.; Chan, S.J.; Steiner, D.F.
Mol.: Endocrinol. 10, 857-866, 1996
A;Title: Structure and expression of the insulin-like peptide receptor from amphioxus.
A;Reference number: Z22346; MUID:96408719; PMID:8813726
A;Accession: T43220
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1363 <PAS>
A;Cross-references: UNIPROT:O02466; EMBL:S83394; NID:gl911771; PID:gl911772; PIDN:AAB508
C;Superfamily: insulin receptor; protein kinase homology
C;Keywords: hormone receptor

Query Match 64.3%; Score 54; DB 2; Length 1363;
Best Local Similarity 61.5%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	CPKVCPECSNC	13
DB	206	CQKVCPECLGNC	218

RESULT 2

AE2094
hypothetical protein alr2308 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2094
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2094
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 <KUR>
A;Cross-references: UNIPROT:Q8YUN1; GB:BA000019; PIDN:BA074007.1; PID:gl7131400; GSPDB:GB
A;Experimental source: strain PCC 7120
C;Genetics: alr2308

Query Match 63.1%; Score 53; DB 2; Length 425;
Best Local Similarity 61.5%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
 || ||| |||
 Db 108 CPDPCPRCEKIC 120

RESULT 3
 JE0142
 C:Superfamily: glutamate synthase small chain - Rhodobacter sphaeroides
 C:Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
 C:Accession: JE0142
 R;Hu, T.; Wu, Y.O.; Song, H.Y.
 Acta Biochim. Biophys. Sin. 29, 294-302, 1997
 A:Title: The nucleotide sequence of gltD gene encoding the small subunit of Rhodobacter
 A:Reference number: JE0142
 A:Accession: JE0142
 A:Molecule type: DNA
 A:Residues: 1-413 <LUA>
 A:Cross-references: UNIPROT:O08340
 A:Note: the authors translated the codon CTG for residue 24 as Lys, CAC for residue 30 as
 A:Gene: gltD
 C:Superfamily: glutamate synthase small chain
 C:Keywords: oxidoreductase

Query Match 61.9%; Score 52; DB 2; Length 413;
 Best Local Similarity 53.3%; Pred. No. 6.8;
 Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPR--RECNSNC 13
 ||| ||| |||
 Db 33 CGRICPQDKCEGNC 47

RESULT 4
 H72230
 C:Superfamily: Thermotoga maritima - Thermotoga maritima (strain MSB8)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: H72230
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: H72230
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-468 <ARN>
 A:Cross-references: UNIPROT:Q9X1X5; GB:AE001806; GB:AE000512; NID:94982196; PIDN:AAD3670
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TW1640
 C:Superfamily: glutamate synthase small chain

Query Match 60.7%; Score 51; DB 2; Length 468;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPR--CESNC 13
 ||| ||| |||
 Db 86 CGRVCPRQVQCESRC 100

RESULT 5
 XKPOT
 C:Superfamily: proteinase inhibitor PTI - potato
 C:Species: Solanum tuberosum (potato)
 C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
 C:Accession: A01318
 R;Hass, G.M.; Hermodson, M.A.; Ryan, C.A.; Gentry, L.

Biochemistry 21, 752-756, 1982
 A:Title: Primary structures of two low molecular weight proteinase inhibitors from potato
 A:Reference number: A90465; MUID:82182863; PMID:7074039
 A:Accession: A01318
 A:Molecule type: protein
 A:Residues: 1-51 <HAS>
 A:Cross-references: UNIPROT:P01079
 A:Note: Arg-38 is probably the site of interaction with trypsin
 C:Superfamily: potato proteinase inhibitor PTI
 C:Keywords: serine proteinase inhibitor

Query Match 59.5%; Score 50; DB 1; Length 51;
 Best Local Similarity 63.8%; Pred. No. 2.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKVCPRCESN 12
 ||| ||| |||
 Db 33 PNVCPRNCDTN 43

RESULT 6
 G95318
 FdxB ferredoxin III [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95318
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: G95318
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-105 <KUR>
 A:Cross-references: UNIPROT:Q92ZK9; GB:AE006469; PIDN:NAK65113.1; PID:G14523551; GSPDB:G
 A:Experimental source: strain 1021, megaplasmid pSymA
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: fdxB
 C:Superfamily: pyruvate synthase subunit porD; ferredoxin 2[4Fe-4S] homology

Query Match 59.5%; Score 50; DB 2; Length 105;
 Best Local Similarity 50.0%; Pred. No. 4.8;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPKVCPRCESN 12
 ||| ||| |||
 Db 86 CARVCPRDCQTH 97

RESULT 7
 JE0352
 mucin MUC5B, tracheobronchial - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
 C:Accession: JE0352
 R;Offner, G.D.; Nunes, D.P.; Keates, A.C.; Afdhal, N.H.; Troxler, R.F.
 Biochem. Biophys. Res. Commun. 251, 350-355, 1998
 A:Title: The amino-terminal sequence of MUC5B contains conserved multifunctional D domain
 A:Reference number: JE0352; MUID:99009274; PMID:9790959
 A:Accession: JE0352
 A:Molecule type: mRNA
 A:Residues: 1-1321 <OFF>

A;Cross-references: GB:AF086604; NID:g3789926; PIDN:AA067545.1; PID:g3789927
 C;Comment: This protein is large multimeric glycoproteins which is secreted by epithelia
 C;Genetics:
 A;Gene: MUC5B

Query Match 59.5%; Score 50; DB 2; Length 1321;
 Best Local Similarity 47.1%; Pred. No. 28;
 Matches 8; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 CPKVCPRC-----ESNC 13

||:|||||
 Db 321 CPCLCPRTCTNMHQNC 337

RESULT 8

T23681

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T23681

R;Matthews, L.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19781

A;Accession: T23681

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1513 <WIL>

A;Cross-references: UNIPROT:O17970; EMBL:Z81573; PIDN:CAB04625.1; GSPDB:GNO0020; CESP:MC

A;Experimental source: clone M02G9

C;Genetics:

A;Gene: CESP:M02G9.1

A;Map position: 2

A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match

Best Local Similarity 59.5%; Score 50; DB 2; Length 1513;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CPKVCPRCECSNC 13

|||||
 Db 1017 CPKACMPCECSNC 1029

RESULT 9

A70477

C;Species: *Aquifex aeolicus*

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Aug-2004

C;Accession: A70477

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O

V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: A70477

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-476 <AQF>

A;Cross-references: UNIPROT:O67845; GB:AE000770; NID:g2984274; PIDN:AA007800.1; PID:g298

A;Experimental source: strain VF5

C;Genetics:

A;Gene: gltD

C;Superfamily: Glutamate synthase, small subunit

Query Match 58.3%; Score 49; DB 2; Length 476;

Best Local Similarity 53.3%; Pred. No. 19;

Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPR-RECSNC 13

||:|||||
 Db 93 CGRVCPRQCEGSC 107

RESULT 10

A46602

C;Species: *Azospirillum brasilense*

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C;Accession: A46602; S10765; S51164

R;Pelanda, R.; Vanoni, M.A.; Perego, M.; Piubelli, L.; Galizzi, A.; Curti, B.; Zanetti,

J. Biol. Chem. 268, 3099-3106, 1993

A;Title: Glutamate synthase genes of the diazotroph *Azospirillum brasilense*. Cloning, se

A;Reference number: A46602; MUID:93155143; PMID:8428988

A;Accession: A46602

A;Molecule type: DNA; protein

A;Residues: 1-481 <PEL>

A;Cross-references: UNIPROT:Q05756; GB:L04300; NID:g289243; PIDN:AAA22178.1; PID:g304130

A;Experimental source: strain Sp7, strain ATCC 29145 and strain Sp6

A;Note: sequence extracted from NCBI backbone (NCBI:124365, NCBI:124371)

R;Vanoni, M.A.; Negri, A.; Zanetti, G.; Ronchi, S.; Curti, B.

Biochim. Biophys. Acta 1039, 374-377, 1990

A;Title: Structural studies on the subunits of glutamate synthase from *Azospirillum bras*

A;Reference number: S10764; MUID:90335272; PMID:2198943

A;Accession: S10765

A;Molecule type: protein

A;Residues: 2-19,'X',21-24;328-332,'A',334-336,'X',338,'X',340,'X',342,'X' <VANI>

R;Vanoni, M.A.; Mazzoni, A.; Pumagalli, P.; Negri, A.; Zanetti, G.; Curti, B.

Eur. J. Biochem. 226, 505-515, 1994

A;Title: Interdomain loops and conformational changes of glutamate synthase as detected

A;Reference number: S51033; MUID:95094808; PMID:8001567

A;Accession: S51164

A;Molecule type: protein

A;Residues: 2-8;475-481 <VAN2>

C;Genetics:

A;Gene: gltD

C;Function:

A;Description: catalyzes the NAD(P)H-dependent reductive transfer of L-glutamine amide g

C;Superfamily: Glutamate synthase, small subunit

C;Keywords: 3Fe-4S; iron-sulfur protein; metalloprotein; NADP; oxidoreductase

F;48,51,56,60,95,99,105,109/Binding site: iron-sulfur clusters (Cys) (covalent) #status

Query Match 58.3%; Score 49; DB 2; Length 481;

Best Local Similarity 46.7%; Pred. No. 19;

Matches 7; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRC--CESNC 13

||:|||||
 Db 95 CGRICPQDLCEGNC 109

RESULT 11

D87696

C;Species: *Caulobacter crescentus*

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004

C;Accession: D87696

R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

n. J.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of *Caulobacter crescentus*.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: D87696

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-481 <STO>

A;Cross-references: UNIPROT:Q9A2F9; GB:AE005673; NID:gl3425352; PIDN:AAK25568.1; GSPDB:G

C;Genetics:

A;Gene: CC3606

C;Superfamily: Glutamate synthase, small subunit

Query Match 58.3%; Score 49; DB 2; Length 481;

Best Local Similarity 46.7%; Pred. No. 19;

Matches 7; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRC--CESNC 13

RESULT:
H85852

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 14:14:16 ; Search time 77.5094 Seconds
(without alignments)
96.503 Million cell updates/sec

Title: US-10-784-537-3
Perfect score: 84
Sequence: 1 CPKVCPRCESNC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	72.6	1359	Q7RM14	Q7rm14 plasmodium
2	54	64.3	331	Q7V9W0	Q7v9w0 prochloroco
3	54	64.3	1363	1 ILPR BRALA	O2466 branchiosto
4	53	63.1	425	Q8YUN1	O8yun1 anabaena sp
5	53	63.1	464	Q8RC72	Q8rc72 thermoanaer
6	53	63.1	466	Q8RBW5	Q8rbw5 thermoanaer
7	53	63.1	649	Q7MBG7	Q7mbg7 wolinnella s
8	53	63.1	672	Q74FU5	Q74fu5 geobacter s
9	53	63.1	672	AAR33841	Aar33841 geobacter s
10	52	61.9	336	Q7UZU5	Q7uzu5 prochloroco
11	52	61.9	631	Q9LT74	Q9lt74 arabidopsis
12	52	61.9	914	Q73KQ0	Q73kq0 treponema d
13	52	61.9	914	AAS12687	Aas12687 treponema
14	51	60.7	352	Q8GLI4	Q8gli4 synchococc
15	51	60.7	462	Q7WTD4	Q7wtd4 porphyromon
16	51	60.7	468	Q9XIX5	Q9xix5 thermotoga
17	51	60.7	763	Q89ZR6	Q89zr6 bacteroides
18	51	60.7	1640	Q78547	Q78547 neurospora
19	50	59.5	51	IP21 SOLTU	P01079 solanum tub
20	50	59.5	105	Q922K9	Q92zk9 rhizobium m
21	50	59.5	154	Q84I56	Q84i56 solanum phu
22	50	59.5	154	AAS01731	Aas01731 solanum p
23	50	59.5	1513	Q17970	Q17970 caenorhabdi
24	50	59.5	5703	1 MUSB HUMAN	Q9hc84 homo sapien
25	49	58.3	177	Q8CAY5	Q8cay5 m mus muscu
26	49	58.3	177	Q9D644	Q9d644 mus musculu
27	49	58.3	204	Q9SDI4	Q9sdi4 capsicum an
28	49	58.3	413	Q08340	Q08340 rhodobacter
29	49	58.3	469	Q8PZ30	Q8pz30 methanosarc
30	49	58.3	476	Q67845	Q67845 aquifex aeo
31	49	58.3	481	1 GLTD_AZOBR	Q05756 azospirillu

32 49 58.3 481 2 Q9A2F9 caulobacter
33 49 58.3 490 2 Q9RNL2 zymomonas m
34 48 57.1 81 2 Q9HAU2 homo sapien
35 48 57.1 132 2 Q7Z4F5 homo sapien
36 48 57.1 132 2 Q9H7G8 homo sapien
37 48 57.1 142 2 Q00485 hydra sp. m
38 48 57.1 174 2 Q9H2Q4 homo sapien
39 48 57.1 348 2 Q7U4K2 synchococc
40 48 57.1 469 2 Q8TJ37 methanosarc
41 48 57.1 470 2 Q748E7 geobacter s
42 48 57.1 470 2 AAR36449 geobacter
43 48 57.1 1035 2 Q6NB27 rhodospseudo
44 48 57.1 1035 2 CAE26122 rhodopseu
45 48 57.1 1412 2 Q8UW84 paralichthy

ALIGNMENTS

RESULT 1

Q7RM14 PRELIMINARY; PRT; 1359 AA.
AC Q7RM14;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Hypothetical protein.
GN Names=PY02196;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_taxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlson J.M., Angiolaeva M.D., Allen J.E., Selengut J.D., Pertea M.,
Silva J.C., Ermolaeva M.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Peterson J.D., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Shallom S.J., van Aken S.E., Sedegah M., Shoaibi A., Cummings L.M.,
Cho J.K., Quackenbush J., Raine J.D., Sinden R.E., Harris M.A.,
Florens L., Yates F.R. III, Rainer J.D., Linder R.E., Vaidya A.B.,
Cunningham D.A., Preiser P.R., Bergman L.W., White O.R.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White M.J.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL0100603; EAA21629.1; -.
DR EMBL; AABL0100603; EAA21629.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1359 AA; 158879 MW; FDBBC1141CCD176A CRC64;

Query Match 72.6%; Score 61; DB 2; Length 1359;

Best Local Similarity 61.5%; Pred. No. 1.4;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13

Db 1180 CPKCKPKCKTQNC 1192

RESULT 2

Q7V9W0 PRELIMINARY; PRT; 331 AA.
AC Q7V9W0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fe-S cluster containing protein.
GN Name=hycB; OrderedLocusNames=Pro1714;

OS Prochlorococcus marinus.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SARG / CCMP 1375 / SS120;
 RX MEDLINE=22810154; PubMed=12917486;
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
 RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
 RA Makarova K.S., Ostrowski M., Otsa S., Robert C., Rogozin I.B.,
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
 RA Wolf Y.I., Hess W.R.;
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
 RT a nearly minimal oxyphototrophic genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
 DR EMBL; AS017166; AAQ00758.1; --
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR Pfam; PF00037; Fez4; 1.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
 KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 331 AA; 36610 MW; C5719BCDCSEFA817 CRC64;
 Query Match 64.3%; Score 54; DB 2; Length 331;
 Best Local Similarity 66.7%; Pred. No. 4.2;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PKVCPRECSNC 13
 Db |||||:
 84 PKVCPKCSRPC 95
 RESULT 3
 ILPR_BRALA STANDARD; PRT; 1363 AA.
 ID 002466;
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin-like peptide receptor precursor (BC 2.7.1.112) (ILP receptor).
 OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7740;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96408719; PubMed=8813726;
 RA Pashmforoush M., Chan S.J., Steiner D.F.;
 RA "Structure and expression of the insulin-like peptide receptor from
 RA amphioxus.";
 RT Mol. Endocrinol. 10:857-866 (1996).
 CC -1- FUNCTION: This receptor binds to the insulin related peptide and
 CC has a tyrosine-protein kinase activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Probable tetramer of 2 alpha and 2 beta chains linked by
 CC disulfide bonds. The alpha chains contribute to the formation of
 CC the ligand-binding domain, while the beta chain carry the kinase
 CC domain [By similarity].
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch.
 CC EMBL; S83394; AAB50848.1; --
 DR PIR; T43220; T43220.
 DR HSSP; P08069; 1JOH.
 DR InterPro; IPR000494; EGFR_L.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow fac recept.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002011; RecepttyrkinaseII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF01030; Recep_L domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00060; FN3; 3.
 DR SMART; SM00261; FU; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00853; FN3; 4.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
 KW transferase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 29
 FT CHAIN 30 716
 FT Insulin-like peptide receptor alpha chain
 FT (Potential).
 FT PROPEP 717 720
 FT CHAIN 721 1363
 FT Insulin-like peptide receptor beta chain
 FT (Potential).
 FT Extracellular (Potential).
 FT Potential.
 FT TRANSMEM 929 949
 FT Cytoplasmic (Potential).
 FT DOMAIN 950 1363
 FT Fibronectin type-III 1.
 FT DOMAIN 475 579
 FT Fibronectin type-III 2.
 FT DOMAIN 588 669
 FT Fibronectin type-III 3.
 FT DOMAIN 712 804
 FT Fibronectin type-III 4.
 FT DOMAIN 810 909
 FT Protein kinase.
 FT DOMAIN 994 1283
 FT NP_BIND 1000 1008
 FT BINDING 1028 1028
 FT ACT_SITE 1148 1148
 FT MOD_RES 1174 1174
 FT Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT CARBOHYD 51 51
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 97 97
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 137 137
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 278 278
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 483 483
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 599 599
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 617 617
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 665 665
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 666 666
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 711 711
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 732 732
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 736 736
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 743 743
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 816 816
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 885 885
 FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 898 898
 FT N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 1363 AA; 154104 MW; 238120B4EAB1ED65 CRC64;
 Query Match 64.3%; Score 54; DB 1; Length 1363;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      1 CPKVCPRCESNC 13
Db      206 CQKVCPSCLGNC 218

RESULT 4
Q8YUN1  PRELIMINARY; PRT; 425 AA.
AC Q8YUN1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-WAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Alr2308 protein.
GN OrderedLocusNames=alr2308;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003589; BAB74007.1; -.
DR PIR; AE2094; AE2094.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4. 1.
DR PRINTS; PR00353; 4Fe4SFRDOXIN.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
DR PSORT; PS00198; 4Fe4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 425 AA; 46348 MW; 7237DCE3EFD6912E CRC64;

Query Match 63.1%; Score 53; DB 2; Length 425;
Best Local Similarity 61.5%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 CPKVCPRCESNC 13
Db      108 CFSDCPRPCEKIC 120

RESULT 5
Q8RC72  PRELIMINARY; PRT; 464 AA.
AC Q8RC72;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE NADPH-dependent glutamate synthase beta chain and related
DE oxidoreductases.
GN Name=Gltd; OrderedLocusNames=TTE0567;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MB4;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013026; AM23842.1; -.

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DR HSSP; Q28943; 1GTE.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR006004; Glut_synth_NADPH.
DR InterPro; IPR009051; Helical_ferredxn.
DR InterPro; IPR000205; NAD_BS.
DR InterPro; IPR00103; Pyridine_redox_2.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00353; 4Fe4SFRDOXIN.
DR PRINTS; PR00419; ADXRDITASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00469; PNDRTTASEII.
DR TIGRFAMs; TIGR01316; gltA; 1.
KW Complete proteome.
SQ SEQUENCE 464 AA; 50786 MW; 9B29DDBBAE97643A CRC64;

Query Match 63.1%; Score 53; DB 2; Length 464;
Best Local Similarity 60.0%; Pred. No. 8.1;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY      1 CPKVCPRPCE--CESNC 13
Db      87 CGRVCPOEQCEKNC 101

RESULT 6
Q8RBW5  PRELIMINARY; PRT; 466 AA.
AC Q8RBW5;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE NADPH-dependent glutamate synthase beta chain and related
DE oxidoreductases.
GN Name=Gltd2; OrderedLocusNames=TTE0693;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MB4;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013037; AM23955.1; -.
DR HSSP; Q28943; 1GTE.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR006004; Glut_synth_NADPH.
DR InterPro; IPR009051; Helical_ferredxn.
DR InterPro; IPR000205; NAD_BS.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRDITASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTTASEI.
DR TIGRFAMs; TIGR01316; gltA; 1.
KW Complete proteome.
SQ SEQUENCE 466 AA; 51088 MW; 20F69C4CDD2F9268 CRC64;

Query Match 63.1%; Score 53; DB 2; Length 466;
Best Local Similarity 60.0%; Pred. No. 8.2;

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Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPRC-ESNC 13

Db 90 CGRVCPCQCEKNC 104

RESULT 7

QYMBG7 PRELIMINARY; PRT; 649 AA.
 ID Q7MBG7;
 AC 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATEDEHYDROGENASE (EC 1.2.1.43)).
 GN Name=FDHB; OrderedLocusNames=WS0477;
 OS Wolinella succinogenes.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Wolinella.
 OX NCBI_TaxID=844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSMZ 1740;
 RX MEDLINE=22882897; PubMed=14500908;
 RA Baar C., Epinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
 RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
 RA Meyer F., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of Wolinella succinogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL; BX571658; CAE09617.1;
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000759; Adrndx_reductase.
 DR InterPro; IPR001327; FAD_Pyr_redox.
 DR InterPro; IPR000103; Pyridine_redox_2.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR PRINTS; PR00419; ADXRDTASEI.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00469; PNDRTASEII.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 649 AA; 72557 MW; CCA1E7589E36650D CRC64;

Query Match 63.1%; Score 53; DB 2; Length 649;

Best Local Similarity 61.5%; Pred. No. 11;

Matches 8; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

QY 1 CPKVCPRC-ESNC 13

Db 194 CGRVCPCQCEKNC 206

RESULT 8

QY4FUS PRELIMINARY; PRT; 672 AA.
 ID Q74FUS;
 AC Q74FUS;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Fe(III) reductase, beta subunit.
 GN Name=sfrB; ORFNames=GSU0510;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

QY 1 CPKVCPRC-ESNC 13

Db 203 CGRVCPCQCEKNC 215

RESULT 10

Q7UZUS PRELIMINARY; PRT; 336 AA.
 ID Q7UZUS;
 AC Q7UZUS;

RA Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments.";
 RL Science 302:1967-1969(2003).
 DR EMBL; AE017180; AAR33841.1; --
 DR TIGR; GSU0510; --
 DR InterPro; IPR000759; Adrndx_reductase.
 DR InterPro; IPR001327; FAD_Pyr_redox.
 DR InterPro; IPR0009051; Helical_ferredxn.
 DR InterPro; IPR000103; Pyridine_redox_2.
 DR InterPro; IPR001100; Pyr_redox.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR PRINTS; PR00419; ADXRDTASEI.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 SQ SEQUENCE 672 AA; 74272 MW; 3779DF2F9AE0D446 CRC64;

Query Match 63.1%; Score 53; DB 2; Length 672;

Best Local Similarity 53.8%; Pred. No. 11;

Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 CPKVCPRC-ESNC 13

Db 203 CGRVCPCQCEKNC 215

RESULT 9

AAR33841 PRELIMINARY; PRT; 672 AA.
 ID AAR33841;
 AC AAR33841;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Fe(III) reductase, beta subunit.
 GN SPRB OR GSU0510.
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments.";
 RL Science 302:1967-1969(2003).
 DR EMBL; AE017208; AAR33841.1; --
 DR TIGR; GSU0510; --
 SQ SEQUENCE 672 AA; 74272 MW; 3779DF2F9AE0D446 CRC64;

Query Match 63.1%; Score 53; DB 2; Length 672;

Best Local Similarity 53.8%; Pred. No. 11;

Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 CPKVCPRC-ESNC 13

Db 203 CGRVCPCQCEKNC 215

RESULT 10

Q7UZUS PRELIMINARY; PRT; 336 AA.
 ID Q7UZUS;
 AC Q7UZUS;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=PM1560;
 OS Prochlorococcus marinus subsp. pastoris (strain COMP 1378 / MED4).
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=59919;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
 RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation.";
 RL Nature 424:1042-1047(2003).
 RL EMBL; BX52094; CAB2019.1; -.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR Pfam; PF00037; Fer4; 1.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
 KW 4Fe-4S; Complete proteome; Hypothetical protein; Iron; Iron-sulfur;
 KW Metal-binding.
 SQ SEQUENCE 336 AA; 37282 MW; CBC53CAGF8A27AB3 CRC64;

 Query Match 61.9%; Score 52; DB 2; Length 336;
 Best Local Similarity 61.5%; Pred. No. 8.5;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

 QY 1 CPKVCPCRECSNC 13
 DB 99 CPSCNCPCEIC 111

 RESULT 11
 Q9LT74 PRELIMINARY; PRT; 631 AA.
 AC Q9LT74;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similarity to late embryogenesis abundant protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20277480; PubMed=108193329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB025624; BAB02467.1; -.
 DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
 DR InterPro; IPR011061; Antihemostatic.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR InterPro; IPR003882; Pistil_extensin.
 DR InterPro; IPR009646; Root_cap.
 DR Pfam; PF06830; Root_cap; 1.
 DR PRINTS; PR01218; PSTLEXTENSIN.

DR PROSITE; PS00119; PA2_ASP; UNKNOWN 1.
 SQ SEQUENCE 631 AA; 66824 MW; 55B52FC65C34C17 CRC64;

 Query Match 61.9%; Score 52; DB 2; Length 631;
 Best Local Similarity 53.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 QY 1 CPKVCPCRECSNC 13
 DB 351 CPADCPSCQVDC 363

 RESULT 12
 Q73KQ0 PRELIMINARY; PRT; 914 AA.
 AC Q73KQ0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Pyridine nucleotide-disulphide oxidoreductase family protein.
 GN OrderedLocusNames=TDE2167;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Seehadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
 RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Grebergeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
 RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
 RA Weinstock G.M., Norris S.J., Fraser C.M., Faulen I.T.;
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 RT with other spirochete genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
 DR EMBL; AB017253; AAS12687.1; -.
 DR TIGR; TDE2167; -.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR000759; Adrmdx_reductase.
 DR InterPro; IPR001327; FAD_pyr_redox.
 DR InterPro; IPR009051; Helical_ferredxn.
 DR InterPro; IPR000103; Pyridine_redox_2.
 DR Pfam; PF00037; Fer4; 2.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR PRINTS; PR00353; 4FE4SFRDOXIN.
 DR PRINTS; PR00419; ADXRDXTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00469; FNDRTASEII.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
 KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 914 AA; 101880 MW; 22E32CA9726D4FBE CRC64;

 Query Match 61.9%; Score 52; DB 2; Length 914;
 Best Local Similarity 61.5%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

 QY 1 CPKVCPCRECSNC 13
 DB 415 CGHVCPCYCEQC 427

 RESULT 13
 AAS12687 PRELIMINARY; PRT; 914 AA.
 ID AAS12687
 AC AAS12687;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Pyridine nucleotide-disulphide oxidoreductase family protein.

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GN TDE2167.
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidson T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J., Durkin S.A.,
RA Daugherty S.C., Shetty J., Shvartsbeyn A., Gebregeorgis E., Geer K.,
RA Tsegaye G., Malek J.A., Ayodeji B., Shatsman S., McLeod M.P.,
RA Xiang Q., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z.,
RA Fraser C.M., Paulsen I.T.;
RA "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AE017253; AAS12687.1; -.
DR TIGR; TDE2167; -.
SQ SEQUENCE 914 AA; 101880 MW; 22E32CA9726D4FBE CRC64;

Query Match 61.9%; Score 52; DB 2; Length 914;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
DB 415 CGHVCPRCEYQC 427

RESULT 14
O8GLI4 PRELIMINARY; PRT; 352 AA.
AC O8GLI4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Light dependent period.
GN Name=ldpA;
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RX MEDLINE=22450571; PubMed=12562813;
RA Katayama M., Kondo T., Xiong J., Golden S.S.;
RA "ldpA encodes an iron-sulfur protein involved in light-dependent
RT modulation of the circadian period in the cyanobacterium Synechococcus
RT elongatus PCC 7942.";
RL J. Bacteriol. 185:1415-1422(2003).
DR EMBL; AY136759; AAN06910.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FE4SFDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 352 AA; 37865 MW; 33614612158F2936 CRC64;

Query Match 60.7%; Score 51; DB 2; Length 352;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CPKVCPRCESNC 13
DB 97 CPTDCPRCERV 109

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RESULT 15

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Q7MTD4
ID Q7MTD4 PRELIMINARY; PRT; 462 AA.
AC Q7MTD4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamate synthase, small subunit.
GN Name=gltd; Ordered locus Names=PG2033;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RA "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL; AE017179; AAO66999.1; -.
DR TIGR; PG2033; -.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR006004; Glut_synth_NADPH.
DR InterPro; IPR002173; PfkB.
DR InterPro; IPR000103; Pyridine redox_2.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRDPTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRDTASEI.
DR PRINTS; PR00469; PNDRDTASEII.
DR TIGRFAMs; TIGR01316; glta; 1.
DR PROSITE; PS00584; PFKB_KINASES_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 462 AA; 49811 MW; 66B2B434EFE7A425 CRC64;

Query Match 60.7%; Score 51; DB 2; Length 462;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 CPKVCPR--CESNC 13
DB 87 CGRVCPOEKQCESRC 101

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